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/tissue type="Human Placenta"  
/lab host="DH10B Tona"  
/clone lib="NIH MGC 147"  
/note="Organ: placenta; Vector: pBluescriptR; Site 1:  
all-XhoI; Site 2: BamH; Oligo-dr primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein, in  
(NIH/NHGRI, National Institutes of Health). Note: This is  
a NIH MGC library."  
BASE COUNT 147 a 246 c 245 g 124 t 9 others  
ORIGIN
```

## Alignment Scores:

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Pred. No.: 1.35e-59 Length: 771  
Score: 892.50 Matches: 170  
Percent Similarity: 88.00% Conservative: 6  
Best Local Similarity: 85.00% Mismatches: 19  
Query Match: 60.51% Indels: 5  
DB: 14 Gaps: 2
```

US-10-047-021-86\_COPY\_28\_303 (1-276) x CB959649 (1-771)

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Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db |||||  
147 CAGGACTCCCCGCCCCAGATCCTAGTCCACCCAGGACAGCTGTTCCAGGGCCCTGGC 206  
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
Db |||||  
207 CCTGCCAGGATGAGTGGCAAGCTCTCAGGCCAGCCACCTCCACCATCCGCTGGTGTGCTG 266  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db |||||  
267 AATGGGCGAGCCCTGAGATGGTGGCCGCCAGCCACACACACACCTCTGCTGATGGGACC 326  
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db |||||  
327 CTTCGTGCTGTACAGCCGCCCTGCCCGGGGACATGCCACAGATGGCCAGGCCCTGTCCACA 386  
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db |||||  
387 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTTGGCAGCGCAGTCAGCAGAGGC 446  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db |||||  
447 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTG 506  
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140  
Db |||||  
507 GCTGTGGTGGGTGAGCAGCTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCC 566  
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThr--- 159  
Db |||||  
567 ACAGTCTCATGTTGGAAGATGGGAACCCCTCGGCCCTCCAGCCCGGAAGGCACACAGTG 626  
Qy 160 ValSerGlyGlySerLeuLeuMetAla-----ArgAlaGluLysSerAspGlu 175  
Db |||||  
627 GTCCGGGGGGGTCCCTNCTGATGCAANGAGCAGAGAAGATGGACGAAGGGGACCCT 686  
Qy 176 ***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArg 195  
Db |||||  
687 ANNCATGTGTGGTGGGCCCANCCACAGCGGCNAGAACCATNAGGGGAGAAAGCCCGCC 746
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Search completed: January 31, 2004, 15:28:25  
Job time : 1681.59 secs

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [rgapbs-r@mail.nih.gov](mailto:rgapbs-r@mail.nih.gov)  
 Tissue Procurement: Invitrogen  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LHAM2364 row: o column: 16  
 High quality sequence stop: 535.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5590503"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_125"  
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;  
 Site1: EcoRV (destroyed); Site2: NotI; RNA source pool  
 of three ovaries, from females ranging in age from 38 to  
 49 YO. Library is oligo-dT primed and directionally cloned  
 (EcoRV site is destroyed upon cloning). Average insert  
 size 2.1 kb, insert size range 1-3.5 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 036."

BASE COUNT 257 a 429 c 326 g 217 t 1 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1.06e-59 Length: 1230  
 Score: 897.00 Matches: 195  
 Percent Similarity: 64.31% Conservative: 14  
 Best Local Similarity: 60.00% Mismatches: 37  
 Query Match: 60.81% Indels: 79  
 DB: 12 Gaps: 10

US-10-047-021-86\_COPY\_28\_303 (1-276) x BM906521 (1-1230)

Qy	1	GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly	20
Db	116	CAGACTCCCGCCGCCAGACTCTAGTCCACCCGAGCAGCAGCTGTTCAGGGCCCTGGC	175
Qy	21	ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu	40
Db	176	CTTGCCAGGATGAGTGCACAGCTTCAGGCAGCCACCTCCACCATCCGCTGGTTCGTG	235
Qy	41	AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr	60
Db	236	AATGGGCAGCCCTTGAGCATGGTGCCTCCAGACCCACACCACTCTCTGCTGATGGGACC	295
Qy	61	LeuLeuLeuGlnProProAlaArgGlyHisIshisapGlyGlnAlaLeuSerThr	80
Db	296	CTTCTGTGCTACAGCCCTCTGCCGGGGACATGCCACGATGCCAGGCCCTGTCCACA	355
Qy	81	AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly	100
Db	356	GACCTGGGTCTACACATGTGAGCCAGCAACCGGCTTGGCAGGCAGTCAGCAGAGGC	415
Qy	101	AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal	120
Db	416	GCTCGGTGTCTGTGGTGTCTCTCCGGAGGATTTCCAGATCCAGCCTCGGACATGGTG	475
Qy	121	AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro	140
Db	476	GCTGTGTGGGTGAGCAGTGTACTCTCGAATGTGGCGCGCCCTGGGGCCACCCAGAGCCC	535
Qy	141	ThrValSerTyrTrpIleAspGlyValProLeuAlaLeuGlnProGlyArgHisThrVal	160



Db 123 TGTGGCGCGCTGGGGCCACCCAGAGCCACAGTCTCATGTGTGAAGATGGAAACCC 182  
Qy 151 LeuAlaLeuGlnProGlyValrGHisThrValSerGlyGlySerLeuLeuMetAlaArgAla 170  
Db 183 CTGGCCCTCCAGCCCGGAGGACACACATGTCTCCGGGGGGTCCCTGCTGATGGCAAGACA 242  
Qy 171 GlutylSerAspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGlu 190  
Db 243 GAGAAGAGTACGAGGAGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAG 302  
Qy 191 SerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeu 210  
Db 303 AGCCGCGCAGCCCGGGTTTCCATCAGAGAGCCCGAGGACTACAGGAGCCCTGTGGAGCTT 362  
Qy 211 LeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGly 230  
Db 363 CTGGCTGTGCAGATTCAGCTGGAAATGTGACACTGTGAACCCGGATCTTCGAGAGGC 422  
Qy 231 ProlylSerProArgProAlaValTrpLeu\*\*\*TrpIlylValSerGlyPro\*\*\*-ArgLeuPr 250  
Db 423 CCCAAGCCTAGACCGCGGTGTGGCTCAGCTGGAAGGTCACTGGGCCCTGTCTGGCCTGCC 482  
Qy 250 AsnLeuThrArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgG1 270  
Db 483 CAATCTTACCGGGCTTGTTCAGGACCCAGACTGCCCGGGAAGCAGGAGCTTCCGGG 542  
Qy 270 YGlnArg 272  
Db 543 GCAGAGG 549  
RESULT 13  
CB961002  
LOCUS  
DEFINITION AGENCOURT 1376127 NIH\_MGC\_147 Homo sapiens cDNA clone  
IMAGE:30343790 5', mRNA sequence.  
ACCESSION CB961002  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 797)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-re@mail.nih.gov  
Tissue Procurement: Dr. Stefan Hansson  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM379 row: a column: 15  
High quality sequence stop: 475.  
Location/Qualifiers  
1. .797  
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/tissue\_type="Human Placenta"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_147"  
/note="Organ: placenta; Vector: pBluescriptR; Site 1:  
ali-XhoI; Site 2: BamH; Oligo-dT primed using primer  
5'-TTTTTTTTTTTNN-3', size-selected for average  
insert size 2.3 kb and normalized to 10^5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein  
(NHGRI/NHGRI, National Institutes of Health). Note: This is  
a NIH\_MGC library."

BASE COUNT 161 a 243 c 260 g 133 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.36e-61 Length: 797  
Score: 918.50 Matches: 190  
Percent Similarity: 91.47% Conservativeness: 3  
Best Local Similarity: 90.05% Mismatches: 10  
Query Match: 62.27% Indels: 8  
DB: 14 Gaps: 2

US-10-047-021-86\_COPY\_28\_303 (1-276) x CB961002 (1-797)

Qy 61 LeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerTh 80  
Db 92 CTCCTGCTCATCATGGCCCTTGCCTGGGAGACATGCCACGATGCCAGGCCCTGTCCAC 151  
Qy 80 rAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgG1 100  
Db 152 AGACCTGGGTGTTCACATGTGAGCCAGCACCGCTTGGCAGCGCATCGCAGAGG 211  
Qy 100 YAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVa 120  
Db 212 CGCTCGGCTGTGTGTGTCTCTCGGGAGGATTTCCAGATCCAGCTCGGGACATGGT 271  
Qy 120 lAlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPr 140  
Db 272 GGCTGTGGTGGTGAGCAGTTTACTCTGGAAATGTGGGCCCTTGGGGCCACCCAGAGCC 331  
Qy 140 oThrValSerTrpTrpIlylSerAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVa 160  
Db 332 CACAGTCTCATGTGTGGAAAGATGGGAAACCTCTGGCCCTCCAGCCCGGAAGGACACACAGT 391  
Qy 160 lSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCy 180  
Db 392 GTCCGGGGGTCTCTGTGATGGCAGAGCAGAGAGTGCAGGAAGGACCTACATGTG 451  
Qy 180 sValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnG1 200  
Db 452 TGTGGCCACCAACAGCAGCAGGACACAGGAGAGCGCCGAGCCCGGGTTTCCATCCAGGA 511  
Qy 200 uProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGlu-AsnV 220  
Db 512 GCCCCAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGCAATTCAGCTGGAAAAATG 571  
Qy 220 alThr-LeuLeuAsn-ProAspProAlaGluGlyProLysProArgProAlaValTrpLe 239  
Db 572 TGACACCTGTGTAACCCCGGATCTCTGAGAGGGGCCCCAACCTAGACGGGGTGTGGCT 631  
Qy 239 u\*\*\*TrpIlylSerGlyPro\*\*\*ArgLeu-ProAsnLeuThrArgProCysSerG 258  
Db 632 CAACTGGAAAGTCACTAGTGGCCCTCTGCTGCCCTTCCCTCCCAATCTTACAGCGGCTTGTGTT 691  
Qy 258 ly-----ProArgLeuProArg 263  
Db 692 CACGAGCCCAAAAATACTGCCCGG 714

RESULT 14  
CB961002  
LOCUS  
DEFINITION AGENCOURT 6620212 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5590503  
5', mRNA sequence.  
ACCESSION BM906521  
VERSION BM906521.1 GI:19356900  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1230)

found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM360 row: n column: 04  
High quality sequence stop: 535.  
Location/Qualifiers

## FEATURES

source

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/db_xref="taxon:9606"
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/tissue_type="pre-eclatmpic placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH MGC 148"
note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT      156 a      262 c      247 g      138 t
ORIGIN
Alignment Scores:
Pred. No.:      4,248-68      Length:      803
Score:          1002.50      Matches:      194
Percent Similarity: 94.84%      Conservative: 8
Best Local Similarity: 91.08%      Mismatches: 7
Query Match:    67.97%      Indels:      4
DB:             14      Gaps:      1
US-10-047-021-86_COPY_28_303 (1-276) x CB997292 (1-803)
QY      1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
DB      119 CAGGACTCCCGCCCCAGATCTTAGTCACCCCGAGGACCAGCTGTTTCAGGGCCCTGGC 178
QY      21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProToThrIleArgTrpLeuLeu 40
DB      179 CCTGCCAGGATGAGCTGCGAGCCTCAGCCAGCCACCTCCACCACATCGCTGTTGCTG 238
QY      41 AenGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
DB      239 AATGGGACGCCCCCTGAGCATGTGTCGCCAGACCCACACACACACCTCTCCCTGATGGGACC 298
QY      61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
DB      299 CTTCTGCTACAGCCCCCTGCCCGGGGACATGCCCAGATGGCCAGGCCCTGTCCACA 358
QY      81 AspLeuGlyValTyThrCysGluAlaSerAenArgLeuGlyThrAlaValSerArgGly 100
DB      359 GACCTGGGTGTACACATGTGAGGCCAGCAACCGCTTGGCAGCGCAGTCAGCAGAGGC 418
QY      101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB      419 GCTCGGCTGTCTGTGGCTGTCTCTCGGAGAGATTTCCAGATCCAGCCTCGGGACATGTG 478
QY      121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
DB      479 GCTGTGTGGGTGACAGTTTACTCTGGATGTGGGCCGCCCTGGGGCCACCCAGAGGCC 538
QY      141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB      539 ACAGTCTCATGTGTGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAAGCACACAGTG 598
QY      161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThyTrpMetCys 180
DB      599 TCCGGGGGGTCCCTCTGATGCAGACGCAAAAGAAAGATGACGAAGGGAACCTACCTGTGT 658
QY      181 ValAlaThrAenSerAlaGlyHis-ArgGluSerArgAlaAla-ArgValSer-IleGln 199
```

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Db      659 GTGGCCACCCACAGCGCAGGACATAGGAGGAGCGCGCAACCCCGGTTTCCCATCCAG 718
QY      200 ---GluProGlnAspTyThrGluProValGlu 209
DB      719 GGAGCCCTAGGAATACCCCGAAGCCTGTGAA 751
RESULT 12
LOCUS   BM914311
DEFINITION AGNCOUT6615385 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5479976
5', mRNA sequence.
ACCESSION BM914311
VERSION   BM914311.1 GI:19364690
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1087)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE    Unpublished
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2002 row: b column: 09
High quality sequence stop: 535.
Location/Qualifiers
1..1087
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5479976"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
note="Organ: spleen; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT      268 a      307 c      352 g      159 t      1 others
ORIGIN
Alignment Scores:
Pred. No.:      1,58-61      Length:      1087
Score:          920.00      Matches:      176
Percent Similarity: 96.17%      Conservative: 0
Best Local Similarity: 96.17%      Mismatches: 6
Query Match:    62.37%      Indels:      1
DB:             12      Gaps:      0
US-10-047-021-86_COPY_28_303 (1-276) x BM914311 (1-1087)
QY      91 AsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGlu 110
DB      3 AACCGCTTGGCAGCGCAGTCAGCAGAGCGCTCGGCTGTCTGTGCTGTCTCTCGGGAG 62
QY      111 AspPheGlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGlu 130
DB      63 GATTTCAGATCCAGCCTCGGACATGCTGCTGTGGGTGAGCAGCTTTACTCTGAA 122
QY      131 CysGlyProProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysPro 150
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Qy 199 nGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgGlnLeuGlu 218
Db 670 GGAGCCCCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTGCCGAATCAGTGGAC 727

RESULT 10
BQ890126 941 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT 7982449 Lupski dorsal root ganglion Homo sapiens cDNA
clone IMAGE:6186214 5', mRNA sequence.
ACCESSION BQ890126
VERSION BQ890126.1 GI:22282140
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13578 row: d column: 23
High quality sequence start: 6
High quality sequence stop: 612.
Location/Qualifiers
1. 941
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 182 a 300 c 309 g 149 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 7.2e-69 Length: 941
Score: 1013.50 Matches: 214
Percent Similarity: 80.07% Conservative: 3
Best Local Similarity: 78.97% Mismatches: 31
Query Match: 68.71% Indels: 24
DB: 13 Gaps: 7

US-10-047-021-86_COPY_28_303 (1-276) x BQ890126 (1-941)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 134 CAGGACTCCCGCCCCAGATCTAGTCCACCCCGGAGGACGAGTGTTCAGGCGCCCTGCG 193

Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeu 40
Db 194 CCGCCAGGATGAGCTGCAAGCCTCAGCCAGCCACCTCCACCATCCGCTGGTGTGCTG 253

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Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisLeuLeuProAspGlyThr 60
Db 254 AATGGGAGCCCTGAGCATGGTCCCGCCAGCCACACACACCTCTCTGCTGATGGGACC 313

Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 314 CTTCTGCTGTACAGCCCTCTGCCCGGGAGCATGCCACGATGGCCAGGCGCTGTCCACA 373

Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 374 GACCTGGGTGTACACATGTGAGCCAGCAACCGCTTGGCAGCGCATGAGGAGGC 433

Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 434 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCTCGGGACATGGTG 493

Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProThrGlyHisProGluPro 140
Db 494 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGCGCCCTGGGGCCACCCAGAGGCC 553

Qy 141 ThrValSerTyrTyrTyrAspGlyValProLeuAlaLeuGlnProGlyArgHis--ThrV 160
Db 554 ACAGTCTCATGTGTGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGACACAGTGG 613

Qy 160 alSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetC 180
Db 614 TCCGGGGGGTCCCTCTGCTGATGTCAGAGCAGAGAGAGTGACAGAGGACCTACATGT 673

Qy 180 YsValAlaThrAsnSerAlaGlyHisArg---GluSerArgAlaAlaArgValSerIleG 199
Db 674 GTGTGGCCACCAACAGCGCAGGACATAAGAGGAGAGCGCGCCAGCCCGGGNTTCCCATC 733

Qy 199 In---GluProGlnAspTyrThrGluProValGluLeuAlaVal-----ArgIleG 216
Db 734 CAGGAGCCCCCGAGACTACAGGAAGCCTGGGGAGCGCTTCCGGG-CTGGGCCGAATTC 792

Qy 216 InLeuGluAsnVal---ThrLeuLeuAsnPro---AspPro--AlaGluGlyProLysPr 233
Db 793 AGCTTGGAAATTTGGTGACCCCTGCTGAACCCGGGGATCTCTTGACAAAGGGGCC--CC 849

Qy 233 oArgPro-----AlaValTrpLeu***Tr 241
Db 850 AAGCGCTAAAAAAGCGGGGGTGGGGGCTCCACCTCGAAAGGGGCAATGGGCCCTTG 909

Qy 241 pLysValSerGlyPro***ArgLeu 249
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RESULT 11
LOCUS AGENCOURT 13623935 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30336795 5', mRNA sequence.
ACCESSION CB997292
VERSION CB997292
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 803)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Stefan Hansson
Email: csapbs-remail.nih.gov
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone Sequencing by: Agencourt Bioscience Corporation
DNA distribution: MGC clone distribution information can be

```



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteuna, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojibori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrim, L.M., Stauble, F., Suzuki, M., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., But, C., Fletcher, C., Fujita, D., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Manzoni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.P., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Wittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409 (6821), 685-690 (2001)  
 MEDLINE 21085660  
 PUBMED 11217851

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 MEDLINE 1217851

6 (bases 1 to 3865)  
 TITLE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Iehi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurthara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission

TITLE

# JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/.

## FEATURES

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### CDS

BASE COUNT 826 a 1188 c 1038 g 813 t  
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 Query Match: 72.03% Indels: 2  
 DB: 11 Gaps: 1

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 DB 118 GATTCTCCACCCAGATCTAGTTTACCCCCAGACCACTACTTACAGGGCTTGGCCCA 177  
 QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuAsn 41  
 DB 178 GCCAAGTAGAGTGCAGATCTCCGCCCAACCACTCCCACTATCCGCTGCTGTAAT 237  
 QY 42 GlyGlnProLeuSerMetValProProaspProHisHisLeuLeuProaspGlyThrLeu 61

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,  
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,  
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,  
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE  
JOURNAL

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

On Dec 10, 2002 this sequence version replaced gi:12836108.  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.

CDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5', GAGAGAGAGCGCGCACTCGAGTCTTTTCTTTTCTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. Second  
strand cDNA was prepared with the primer adapter of sequences [5',  
GAGAGAGAGAGGATCAAGAGCTCAATTAATTAACCCCGCCCC 3']. cDNA was  
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:  
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FEATURES  
source

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## CDS

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## ORIGIN

802 a 1115 c 1011 g 761 t

## Alignment Scores:

Pred. No.: 5,9e-72 Length: 3689  
Score: 1062.50 Matches: 204  
Percent Similarity: 83.52% Conservative: 24

Best Local Similarity: 74.73% Mismatches: 43  
Query Match: 72.03% Indels: 2  
DB: 11 Gaps: 1

US-10-047-021-86\_COPY\_28\_303 (1-276) x AK004723 (1-3689)

QY 2 AspSerProGlnInLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21  
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DB 541 TCGGTCTCATGTGGTGAAGAGCGGAAACCCCTGGTCTCTCCAGCCAGGAGGCGCAGTA 600  
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu---ThrTyMetCys 180  
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QY 181 ValAlaThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
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DB 901 AGGTCCCCCAGGACCAAGGATCTCCATGTGAGCAGAGG 937

## RESULT 8

AK087355 3865 bp mRNA linear HTC 05-DEC-2002  
LOCUS Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched  
DEFINITION library, clone:E030049D17 product:similar to MAGIC ROUNDABOUT [Homo  
sapiens], full insert sequence.

## ACCESSION

AK087355  
AK087355.1 GI:26352439  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus



## Alignment Scores:

Pred. No.: 3, 48e-74 Length: 860  
 Score: 1081.50 Matches: 215  
 Percent Similarity: 79.78% Conservatives: 2  
 Best Local Similarity: 79.04% Mismatches: 11  
 Query Match: 73.32% Indels: 44  
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US-10-047-021-86\_COPY\_28\_303 (1-276) x CB996189 (1-860)

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 Qy 240 \*TrrLysValSerGlyPro\*\*\*Arg-----LeuPr 250  
 Db 747 -TGGGAGCTTTCTGGCGCTGTGCGAATTTTCAGCTGGGTAAATAATGTTGACACCTTGCC 805  
 Qy 250 o---AsnLeuThrArgProCys---SerGlyPro 259  
 Db 806 TGGAAACCCCGGGAATCCCTCCAGAGAGGCGCC 839

## RESULT 7

AK004723

LOCUS

DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200012D01 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.

## ACCESSION

AK004723.2 GI:26334429

## KEYWORDS

HTC; CAP trapper.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

## REFERENCE

## AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

## REFERENCE

## AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

## REFERENCE

## AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,

Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,

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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,

Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,

Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.

and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

## REFERENCE

## AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3689)

## REFERENCE

## AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,

Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,

Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishii, K.,

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,

Saito, H., Saito, R., Sakai, C., Sano, H., Sasaki, D.,

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 826)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM348 row: c column: 24

High quality sequence stop: 637.

Location/Qualifiers

1..826

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30331943"

/tissue\_type="pre-eclatptic placenta"

/lab\_host="DH10B Tona"

/clone\_lib="NIH MGC 148"

/note="Organ: placenta; Vector: pBluescriptR; Site 1:

all-XhoI; Site 2: BamH; Library is oligo-dT primed and

directionally cloned using primer

5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert

size 2.3 kb and normalized to ROT 5. This is a primary

library enriched for full-length clones and constructed

using the Cap-trapper method (Carninci, in preparation).

Library constructed by M. Brownstein (NHGRI, NHGRI,

National Institutes of Health). Note: this is a NIH\_MGC

Library."

BASE COUNT 160 a 266 c 261 g 138 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-75 Length: 826

Score: 1101.00 Matches: 216

Percent Similarity: 91.98% Conservative: 2

Best Local Similarity: 91.14% Mismatches: 14

Query Match: 74.64% Indels: 5

DB: 14 Gaps: 2

US-10-047-021-86\_COPY\_28\_303 (1-276) x CB994099 (1-826)

Qy 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20

Db 119 CAGGACTCCCGCCCGAGATCTAGTCCACCCCGAGGACGAGCTGTCACGGGCGCTGGC 178

Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrThrLeuLeuLeu 40

Db 179 CCTGCGAGGATGAGTGGCGAGCTCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 238

Qy 41 AenGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60

Db 239 AATGGGAGGCGCCCTGAGCATGGTGGCCCGAGCCAGCCAGCCAGCCAGCCAGCCAGCC 298

Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80

Db 299 CTTCTGTGCTACAGCCCGCTGCGCGGAGCATGCCACGATGCGCGCCCTGTCCACA 358

Qy 81 AspLeuGlyValThrThrCysGluAlaSerHisArgLeuGlyThrAlaValSerArgGly 100

Db 359 GACCTGGGTGTCTACATGTGAGCCAGCAACCGCTTGGACGGCAGTCAGCAGAGGC 418

Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120

Db 419 GCTCGGCTGTCTGTGGCTGTCTCGGAGGAGATTTCAGATCCAGCTCGGGAGCATGGTG 478

Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProThrGlyHisProGluPro 140

Db 479 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGCGCGCTGGGGCCACCCAGAGCCC 538

Qy 141 ThrValSerThrTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160

Db 539 ACAGTCTCATGTGTGAAGATGGGAACCCCTGCGCCCTCCAGCCCGGAAGGCACACAGTG 598

Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*ThrTyrMetCys 180

Db 599 TCCGGGGGCTCCCTGCTGATGGCAAGACAGAGAGAGTGCAGAAAGACCTTACATGTGT 658

Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200

Db 659 GTGGCCCAACACAGCGCAAGACATANGAGAGCGCGCCGCCCGGGTTTTCATCCAGGAG 718

Qy 201 -ProGlnAspTyrThr-GluProVal-GluLeuLeu---AlaValArgIleGlnLeuGlu 218

Db 719 CCCCAGGACTACACGGGAGCTGTGGGAGCTTCTGGGCTGTGGCAATTTTCAGCTGGGAA 778

Qy 219 AsnValThrLeuLeu---AsnProAspProAlaGluGlyProLys 232

Db 779 AATGTGACACTGGCTGGAAACCCCGATCTCTGGCAAGGGGCCCA 823

RESULT 6

CB996189 860 bp mRNA linear EST 01-MAY-2003

AGENCOURT 13622686 NIH\_MGC\_148 Homo sapiens cDNA clone

IMAGE:30337143 5', mRNA sequence.

CB996189

CB996189.1 GI:30290709

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 860)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM361 row: 1 column: 16

High quality sequence stop: 578.

Location/Qualifiers

1..860

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30337143"

/tissue\_type="pre-eclatptic placenta"

/lab\_host="DH10B Tona"

/clone\_lib="NIH MGC 148"

/note="Organ: placenta; Vector: pBluescriptR; Site 1:

all-XhoI; Site 2: BamH; Library is oligo-dT primed and

directionally cloned using primer

5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert

size 2.3 kb and normalized to ROT 5. This is a primary

library enriched for full-length clones and constructed

using the Cap-trapper method (Carninci, in preparation).

Library constructed by M. Brownstein (NHGRI, NHGRI,

National Institutes of Health). Note: this is a NIH\_MGC

Library."

BASE COUNT 169 a 279 c 267 g 144 t 1 others

ORIGIN





## ORIGIN

Alignment Scores:  
 Pred. No.: 1,18-97 Length: 1201  
 Score: 1387.00 Matches: 263  
 Percent Similarity: 96.35% Conservative: 1  
 Best Local Similarity: 95.99% Mismatches: 8  
 Query Match: 94.03% Indels: 2  
 DB: 9 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x AL553360 (1-1201)

Qy 1 GlnAspSerProGlnInLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
 Db 162 CAGGACTCCCGCCAGATCTAGTCCACCCAGGACCATGTTCCAGGCGCCCTGGC 221  
 Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
 Db 222 CCGCAGGATGAGTGCACGCTCAGCCAGCCCTCCAGCCAGCCCTCCAGCATCCGCTGGTGTG 281  
 Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
 Db 282 AATGGCAGCCCTGAGCATGGTCCCGGACCCAGCCACCATCTCTGCTGATGGGACC 341  
 Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
 Db 342 CTTCCTGCTACAGCCCTCCCGGGGACATGCCACGATGGCCAGCCCTGTCCACA 401  
 Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
 Db 402 GACCTGGGTGTACACATGTGAGCCAGCAACCGCTTGGCAGCGCATGTAGCAGAGGC 461  
 Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
 Db 462 GCTGGCTGTCTGGCTGTCTCGGAGGATTTCCAGATCCAGCCCTCGGACATGGTG 521  
 Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140  
 Db 522 GCTGGTGGTGAGCAGTTACTCTGAATGTGGCGCCCTGGGGCCACCCAGAGCCC 581  
 Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVa 160  
 Db 582 ACAGTCTCATGTGGAAGATGGAAACCCCTGGCCCTCCACGCGCGGAGGCACACAGT 641  
 Qy 160 LserGlyCysLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTrpMetCy 180  
 Db 642 GTCCGGGGGTCCTCTGTGATGGCAAGAGCAGAGAGATGACGAAGGACCTCATGTG 701  
 Qy 180 sValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGln 200  
 Db 702 TGTGGCCACCAACAGCGAGCATAGGAGAGCGCGCCACCCGGGTTTCATCCAGGA 761  
 Qy 200 uProGlnAspTrpThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVa 220  
 Db 762 GCCCAGGACTACAGGAGCTGTGGAGCTCTGGCTGTGGCAATTCAGCTGGAAATGT 821  
 Qy 220 lThrLeuLeuAsnProAspProAlaGluClyProLysProArgProAlaValTrpLeu\*\* 240  
 Db 822 GACACTGTGTAACCGGATCTTCAGAGGGGCCCAAGCCTAGACCGCGGTGTGGCTCAG 881  
 Qy 240 \*TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProA 260  
 Db 882 CTGGAGGTCTAGTGGGCTCTGTGGCTTGGCCATCTTACACGGCTTGTTCAGGACCCA 941  
 Qy 260 rgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272  
 Db 942 GACTGCCCGGGAGGCCAGGAGCTCTGTGGGAGAGG 979

## RESULT 3

BM921911 1019 bp mRNA linear EST 12-MAR-2002  
 LOCUS AGENCOURT 6706908 NIH\_MGC\_115 Homo sapiens CDNA clone IMAGE:5753515  
 DEFINITION 5', mRNA sequence.

## ACCESSION

BM921911 GI:19372290

## VERSION

BM921911.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 1019)

## AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM12789 row: 9 column: 20

High quality sequence stop: 697.

Location/Qualifiers

1..1019

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5753515"

/lab\_host="DH10B"

/note="SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH\_MGC library."

BASE COUNT 201 a 331 c 321 g 162 t 4 others

ORIGIN

Alignment Scores:

Pred. No.: 1,63e-94 Length: 1019

Score: 1345.00 Matches: 254

Percent Similarity: 97.70% Conservative: 1

Best Local Similarity: 97.32% Mismatches: 4

Query Match: 91.19% Indels: 2

DB: 12 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x BM921911 (1-1019)

Qy 8 LeuValHisProGlnAspGlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg 27

Db 16 CTAGTCCACCCAGGACCATGTTCCAGGCGCCCTGGCCCTGCGAGGATGAGCTGCCAA 75

Qy 28 AlaSerGlyGlnProProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMet 47

Db 76 GCCTCAGGCCAGCCACCTCCACCATCGCTGGTGTGTAATGGGCGAGCCCTGAGCATG 135

Qy 48 ValProProAspProHisHisLeuLeuProAspGlyThrLeuLeuGlnProPro 67

Db 136 GTGCCCCCAGACCCACACCATCTCTGCTGATGGACCTCTGCTCTACAGCCCCCT 195

Qy 68 AlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyValThrCys 87

Db 196 GCCCGGGGACATGCCACGATGGCCAGGCGCTGTCCACAGACCTGGGTGTCTACATGT 255

Qy 88 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 107

Db 256 GAGGCCAGCAACCGCTTGGCAGCGCATGTCAGCAGAGCGCGCTCGCTGTCTGTGCTGTC 315

# AUTHORS TITLE JOURNAL

Strausberg, R.  
Direct Submission  
Submitted (01-NOV-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

## REMARK COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Invitrogen  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amadane@systemsbio.org](mailto:amadane@systemsbio.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAP Plate: 84 Row: i Column: 5  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis, Genomescan gene prediction  
This clone has the following problem: frame shifted.

## FEATURES

source

1. 3758  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5590503"  
/tissue\_type="Ovary, pooled from 3 adults"  
/clone\_lib="NIH MGC\_125"  
/lab\_host="DH10B"  
/note="vector: pCMV-SPORT6"  
772 a 1232 c 1046 g 708 t

BASE COUNT  
ORIGIN

Alignment Scores:  
Pred. No.: 1.41e-100 Length: 3758  
Score: 1432.00 Matches: 268  
Percent Similarity: 98.53% Conservative: 1  
Best Local Similarity: 98.17% Mismatches: 3  
Query Match: 97.08% Indels: 1  
DB: 11 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x BC039602 (1-3758)

Qy 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db 110 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACGAGCTTCCAGGCGCCCTGGC 169  
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40  
Db 170 CTTGCCAGGATGAGTGCACAGCTTCAGGCGAGCCACCTCCACCATCCGCTGGTTGCTG 229  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db 230 AATGGGAGCCCCCTGAGGATGTGCCCCCAGACCCACACCATCTCTCCCTGATGGGACC 289  
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db 290 CTTCTGCTGTACAGCCCCCTGCCCGGGGACATGCCCCAGATGGCCAGGCTGTCCACA 349  
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db 350 GACCTGGGTGTACACATGTGAGGCCAGCAACCGCTTGGCAGCGAGTCAGCAGAGGC 409  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db 410 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCTCCGGACATGGTG 469  
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140

Db 470 GCTGTGTGTGGTGGAGCAGTTTACTCTGGAATGTGGCGCGCTTGGGGCCACCCAGAGCCC 529  
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160  
Db 530 ACAGTCTCATGTGTGGAAAGATGGAAACCCCTGCGCTCCAGCCCGGAGGCACACAGTG 589  
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyMetCys 180  
Db 590 TCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTACAGNAGGAGCTACATGTGT 649  
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
Db 650 GTGGCCACCAACAGCGCAGACATAGGAGAGCGCGCAGCGCGGTTCATCCAGGAG 709  
Qy 201 ProGlnAspTrpThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220  
Db 710 CCCAGGACTACACGGAGCTGTGGAGCTTCTGCTGTGGAAATTCAGCTGGAATATGTG 769  
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\* 240  
Db 770 AACTGTGTAACCGGATCTGCGAGAGGCGCCCAAGCCTAGACCGCGGTGTGCTCAGC 829  
Qy 241 TrpLysValSerGlyPro\*\*\*-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260  
Db 830 TGAAGGTCAGTGGCCCTGCTGCGCTGCCCAATCTTACACGGCTTGTTCAGGACCCAG 889  
Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272  
Db 890 ACTGCCCCGGAGGCCAGGAGCTCCGTGGGCAGAG 926  
RESULT 2  
LOCUS AL553360 1201 bp mRNA linear EST 31-MAY-2003  
DEFINITION AL553360 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
clone CSODI075YP13 5-PRIME, mRNA sequence.  
ACCESSION AL553360  
VERSION AL553360.2 GI:31275174  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length CDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12893123.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 6206.r For  
more information about this cluster, see  
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI075CH07QPI&cluster=6206.r>. Contact :  
Feng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSODI075CH07QPI.  
Location/Qualifiers  
1. 1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODI075YP13"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT 236 a 348 c 369 g 212 t 36 others

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2004, 12:28:30 ; Search time 1674.59 Seconds  
(without alignments)  
4005.776 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303  
Perfect score: 1475  
Sequence: 1 QDSPPIVHPQDLQFGPG.....SGPRLPREARELRQRRNTG 276

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlp  
-Q=/Cgn2\_1/USPTO\_spool\_p/US10047021/runat\_30012004\_145453\_24574/app\_query.fasta\_1.910  
-DB=EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10047021.QCGN 1 1 4399 @runat\_30012004\_145453\_24574 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_ges\_hum:\*  
18: em\_ges\_inv:\*  
19: em\_ges\_pln:\*  
20: em\_ges\_vrt:\*  
21: em\_ges\_fun:\*  
22: em\_ges\_mam:\*  
23: em\_ges\_mus:\*  
24: em\_ges\_pro:\*  
25: em\_ges\_rod:\*  
26: em\_ges\_phg:\*  
27: em\_ges\_vrl:\*  
28: gb\_ges1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1432	97.1	3758	11	BC039602	BC039602 Homo sapi
2	1387	94.0	1201	9	AL553360	AL553360 AL553360
3	1345	91.2	1019	12	BM921911	BM921911 AGENCOURT
4	1132	76.7	922	13	BX418142	BX418142 BX418142
5	1101	74.6	826	14	CB994099	CB994099 AGENCOURT
6	1081.5	73.3	860	14	CB996189	CB996189 AGENCOURT
7	1062.5	72.0	3689	11	AK004723	AK004723 Mus muscu
8	1062.5	72.0	3865	11	AK087355	AK087355 Mus muscu
9	1029.5	69.8	729	12	BI762862	BI762862 603048384
10	1013.5	68.7	941	13	B0890126	B0890126 AGENCOURT
11	1002.5	68.0	803	14	CB997292	CB997292 AGENCOURT
12	920	62.4	1087	12	BM914311	BM914311 AGENCOURT
13	918.5	62.3	797	14	CB961002	CB961002 AGENCOURT
14	897	60.8	1230	12	BM906521	BM906521 AGENCOURT
15	892.5	60.5	771	14	CB959649	CB959649 AGENCOURT
16	891.5	60.4	610	10	BG745318	BG745318 602723637
17	884	59.9	798	14	CB961529	CB961529 AGENCOURT
18	847	57.4	688	14	CB961818	CB961818 AGENCOURT
19	803	54.4	558	9	AL602474	AL602474 DKFZp6860
20	782	53.0	570	10	BE233526	BE233526 139756 MA
21	742.5	50.3	662	14	BY727209	BY727209 BY727209
22	732	49.6	502	13	BX474842	BX474842 DKFZp686M
23	704.5	47.8	620	10	BB664621	BB664621 BB664621
24	656	44.5	532	13	BX475138	BX475138 DKFZp6860
25	651	44.1	526	14	CA394658	CA394658 ccs4c07.Y
26	647.5	43.9	631	10	BE376779	BE376779 601227331
27	642	43.5	501	13	BX474746	BX474746 DKFZp686B
28	577.5	39.2	529	4	BX520802	BX520802 RZPD Mus
29	576.5	39.1	551	9	AI116483	AI116483 ud74c05.Y
30	574.5	38.9	557	14	BY704924	BY704924 BY704924
31	574	38.9	344	9	AA577940	AA577940 nl20d01.s
32	567	38.4	438	13	BX475177	BX475177 DKFZp686F
33	566	38.4	450	9	AL039859	AL039859 DKFZp643AE
34	529	35.9	532	12	BI159602	BI159602 602920006
35	527	35.7	424	13	BX475172	BX475172 Homo sapi
36	527	35.7	426	2	HS085795	HS085795 Homo sapi
37	489.5	33.2	455	10	BB839755	BB839755 BB839755
38	452.5	30.7	1257	14	CB993951	CB993951 AGENCOURT
39	447	30.3	555	12	BI836220	BI836220 603085778
40	428.5	29.1	379	10	BB871780	BB871780 BB871780
41	426.5	28.9	441	13	BY285423	BY285423 BY285423
42	424.5	28.8	444	13	BY270114	BY270114 BY270114
43	412.5	28.0	782	14	CB527120	CB527120 UI-M-PYO-
44	409.5	27.8	586	14	CB585643	CB585643 AMGNNUC:N
45	405.5	27.5	781	14	CB527493	CB527493 UI-M-PYO-

ALIGNMENTS

RESULT 1  
LOCUS BC039602 3758 bp mRNA linear HTC 06-NOV-2002  
DEFINITION Homo sapiens, Similar to roundabout homolog 4, magic roundabout  
(Drosophila), clone IMAGE:5590503, mRNA.  
ACCESSION BC039602  
VERSION BC039602.1 GI:24660430  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3758)

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:51:24 ; Search time 29.0777 Seconds  
(without alignments)  
2449.385 Million cell updates/sec

Title: us-10-047-021-86\_copy\_28\_303

Perfect score: 1475

Sequence: 1 QDSPPQILVHPDQLFGPG.....SGPRLPREARELQRENTG 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*\*

1: sp\_archaea:\*\*

2: sp\_bacteria:\*\*

3: sp\_fungi:\*\*

4: sp\_human:\*\*

5: sp\_invertebrate:\*\*

6: sp\_mammal:\*\*

7: sp\_mhc:\*\*

8: sp\_organelle:\*\*

9: sp\_phase:\*\*

10: sp\_plant:\*\*

11: sp\_rodent:\*\*

12: sp\_virus:\*\*

13: sp\_vertebrate:\*\*

14: sp\_unclassified:\*\*

15: sp\_rvirus:\*\*

16: sp\_bacteriap:\*\*

17: sp\_archaeap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1311	88.9	1007	4 Q8WZ75	Q8WZ75 homo sapien
2	1303	88.3	792	4 Q6JW6	Q6JW6 homo sapien
3	1029.5	69.8	1016	11 Q8C310	Q8C310 mus musculus
4	748	50.7	702	4 Q8TEG1	Q8TEG1 homo sapien
5	448.5	30.4	1034	4 Q96MS0	Q96MS0 homo sapien
6	448.5	30.4	1651	11 Q55005	Q55005 rattus norv
7	445.5	30.3	1651	4 Q9Y6N7	Q9Y6N7 homo sapien
8	445.5	30.2	1612	11 Q89026	Q89026 mus musculus
9	442.5	30.0	330	13 Q90242	Q90242 gallus gall
10	432	29.3	1614	13 Q8UVD7	Q8UVD7 xenopus lae
11	420.5	28.5	1513	13 Q90270	Q90270 brachydanio
12	414.5	28.1	1344	11 Q92214	Q92214 mus musculus
13	404.5	27.4	1380	4 Q9HCK4	Q9HCK4 homo sapien
14	403.5	27.4	333	13 Q90241	Q90241 gallus gall
15	401.5	27.2	1389	13 Q90269	Q90269 brachydanio
16	401.5	27.2	1419	13 Q98SW3	Q98SW3 brachydanio

17	400.5	27.2	1675	13 Q98SW4	Q98SW4 brachydanio
18	395.5	26.8	1395	5 Q9W213	Q9W213 drosophila
19	395.5	26.8	1395	5 Q44924	Q44924 drosophila
20	394.5	26.7	227	11 Q8BJ59	Q8BJ59 mus musculus
21	394	26.7	1342	5 Q8GPP6	Q8GPP6 drosophila
22	394	26.7	1342	5 Q9VZ27	Q9VZ27 drosophila
23	354.5	24.0	1269	5 O01632	O01632 caenorhabdi
24	354.5	24.0	1273	5 O44928	O44928 caenorhabdi
25	348.5	23.6	376	13 Q90271	Q90271 brachydanio
26	346	23.5	1060	11 Q90213	Q90213 rattus norv
27	340	23.1	1406	5 Q8GPP7	Q8GPP7 drosophila
28	340	23.1	1483	5 Q9VQ08	Q9VQ08 drosophila
29	267.5	18.1	1496	4 Q9VQ08	Q9VQ08 homo sapien
30	261.5	17.7	1151	11 Q9QVNS	Q9QVNS rattus norv
31	261.5	17.7	1174	11 Q91260	Q91260 rattus norv
32	261.5	17.7	1217	11 P97685	P97685 rattus norv
33	260.5	17.7	298	4 Q96HT1	Q96HT1 homo sapien
34	260.5	17.7	1041	4 Q94856	Q94856 homo sapien
35	259	17.6	1311	5 Q961K8	Q961K8 drosophila
36	259	17.6	1527	5 Q9VZ24	Q9VZ24 drosophila
37	253.5	17.2	1028	11 P97528	P97528 rattus norv
38	253	17.2	1535	5 Q23991	Q23991 drosophila
39	252.5	17.1	498	11 Q8BRT6	Q8BRT6 mus musculus
40	252.5	17.1	705	11 Q8CBD3	Q8CBD3 mus musculus
41	251	17.0	1272	13 Q90924	Q90924 gallus gall
42	251	17.0	1369	13 O42414	O42414 gallus gall
43	248.5	16.8	1026	11 Q62845	Q62845 rattus norv
44	245.5	16.6	1028	11 Q8C6X1	Q8C6X1 mus musculus
45	245	16.6	1427	13 Q91562	Q91562 xenopus lae

#### ALIGNMENTS

#### RESULT 1

Q8WZ75	ID	Q8WZ75	PRELIMINARY;	PRT;	1007 AA.
AC	Q8WZ75;				
DT	01-MAR-2002	(TrEMBLrel. 20, Created)			
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)			
DE	Magic roundabout.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20530916; PubMed=11076864;				
RA	Huminecki L., Bicknell R.;				
RT	"In silico cloning of novel endothelial-specific genes.";				
RL	Genome Res. 10:1796-1806(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Huminecki L., Bicknell R.;				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF361473; AAL31867.1;				
DR	Genew; HGNC:17985; ROBO4				
DR	InterPro; IPR003961; FN_III.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003598; Ig_c2.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00041; fn3; 2.				
DR	Pfam; PF00047; ig; 2.				
DR	SMART; SM00060; FN3; 2.				
DR	SMART; SM00408; IGC2; 1.				
DR	PROSITE; PS00835; IG_LIKE; 2.				
KW	Immunoglobulin domain.				
SQ	SEQUENCE 1007 AA; 107457 MW; E43F246C59BE1415 CRC64;				

Query Match 88.9%; Score 1311; DB 4; Length 1007;  
Best Local Similarity 98.8%; Pred. No. 1e-104;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
 DB 28 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87  
 QY 61 LLLQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARLSAVLREDFOIQRDMV 120  
 DB 88 LLLQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARLSAVLREDFOIQRDMV 147  
 QY 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 180  
 DB 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 207  
 QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 240  
 DB 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 267  
 QY 241 WKVSGP 246  
 DB 268 WKVSGP 273  
 RESULT 2  
 Q96JV6 PRELIMINARY; PRT; 792 AA.  
 AC Q96JV6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein FLJ14946.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Isoqai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
 RA Wakamatsu A., Nakamura Y., Nagahari K., Maeuho Y., Oshima A.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK027852; BAB55411.1;  
 DR InterPro; IPR003961; FN111.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00041; fn3.2.  
 DR Pfam; PF00047; ig.2.  
 DR SMART; SM00060; FN3.2.  
 DR SMART; SM00408; IGC2.1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 KW Hypothetical protein; Immunoglobulin domain.  
 SQ SEQUENCE 792 AA; 85419 MW; FC6DC05275B7B234 CRC64;

Query Match 88.3%; Score 1303; DB 4; Length 792;  
 Best Local Similarity 98.4%; Pred. No. 3.7e-104;  
 Matches 242; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
 DB 28 QDSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87  
 QY 61 LLLQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARLSAVLREDFOIQRDMV 120  
 DB 88 LLLQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARLSAVLREDFOIQRDMV 147  
 QY 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 180  
 DB 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 207

QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 240  
 DB 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 267  
 QY 241 WKVSGP 246  
 DB 268 WKVSGP 273  
 RESULT 3  
 Q8C310 PRELIMINARY; PRT; 1016 AA.  
 AC Q8C310;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Similar to MAGIC ROUNDABOUT.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RC MEDLINE=22354683; PubMed=12466851;  
 RA The PANTOM Consortium.  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK087355; BAC39850.1;  
 SQ SEQUENCE 1016 AA; 108461 MW; DE70683C63AEC8E CRC64;

Query Match 69.8%; Score 1029.5; DB 11; Length 1016;  
 Best Local Similarity 78.5%; Pred. No. 2.2e-80;  
 Matches 193; Conservative 20; Mismatches 32; Indels 1; Gaps 1;  
 QY 2 DSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 61  
 DB 39 DSPQILVHPDQDLFOGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 98  
 QY 62 LLLQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARLSAVLREDFOIQRDMV 120  
 DB 99 LLLQPPARGHAHDGQALSTDLGVYTCESNRGLTAVSRGARLSAVLREDFOIQRDMV 158  
 QY 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 180  
 DB 159 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGSLLMARAEKSDXTYMC 218  
 QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 240  
 DB 219 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAVWLX 278  
 QY 241 WKVSGP 246  
 DB 279 WKVSGP 284

RESULT 4  
 Q8TEG1 PRELIMINARY; PRT; 702 AA.  
 AC Q8TEG1;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE FLJ00236 protein (Fragment).  
 GN FLJ00236.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RL spleen.";
DR Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074163; BAB84989.1; -
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON TER
SQ SEQUENCE 702 AA; 75340 MW; D668FEE4BCAFDCC6 CRC64;

Query Match 50.7%; Score 748; DB 4; Length 702;
Best Local Similarity 96.5%; Pred. No. 3e-56;
Matches 139; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 103 LSVAVLRDFOIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHVTSG 162
Db 20 LLIMVLRDFOIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHVTSG 79

Qy 163 GSLLMARAEKSDXTMYCVATNSAGHRESRAARVSIQEPDQYTPVELLAVRIQLENTVL 222
Db 80 GSLLMARAEKSDXTMYCVATNSAGHRESRAARVSIQEPDQYTPVELLAVRIQLENTVL 139

Qy 223 LNPDPAGPKPRPAVWLXKWSGP 246
Db 140 LNPDPAGPKPRPAVWLXKWSGP 163

RESULT 5
ID Q96MS0 PRELIMINARY; PRT; 1034 AA.
AC Q96MS0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ31982.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Nimmiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NSDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056544; BAB71212.1; -
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 1034 AA; 110723 MW; 09E13C7B424F7E30 CRC64;
```

```
Query Match 30.4%; Score 448.5; DB 4; Length 1034;
Best Local Similarity 43.1%; Pred. No. 3.8e-30;
Matches 109; Conservative 23; Mismatches 90; Indels 31; Gaps 8;

Qy 1 QDSPPQILVHPQDQLFGQPGPARMSCRAGSQPPPTIRWLNGQPLSMVPPDP--HH-LLP 57
Db 60 EDAMPRIVEQPPDLLVSRGEPATLPCRAEGRPRNIEMYNKNGARVATVREDPRHRLLLP 119

Qy 58 DGTLLILLOPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGRLSVAVLREDFOIQPR 117
Db 120 SGALFF---PRIVH---GRRARPDEGYTCVARNYLGAASRNASLEVAVLDRFQSPG 173

Qy 118 DMVAVGGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHVTSGGSLLMARAEKSDXT 177
Db 174 NVVAVGEPAVLECVPPRGHPGPSVSRKDGARLKEEGRTITIRGKLLMMSHTLKSAGM 233

Qy 178 YMCVATNSAGHRESRAARVSIQEPDQYTPVELLAVRIQLENTVLNPPDAE----- 229
Db 234 YVCVASNMAGERESAAMVMLRPSFLRRPV-----NQVLADAPVTFLCEVKG 283

Qy 230 GPKPRPAVWLXWK 242
Db 284 DPPP-----LRWR 292

RESULT 6
ID O55005 PRELIMINARY; PRT; 1651 AA.
AC O55005;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Transmembrane receptor Robol.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=98117249; PubMed=9458045;
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.;
RT "Roundabout controls axon crossing of the CNS midline and defines a
RT novel subfamily of evolutionarily conserved guidance receptors.";
RL Cell 92:205-215 (1998)
DR EMBL; AF041082; AAC39960.1; -
DR HSSP; P56276; 1TLK.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 1651 AA; 180747 MW; FA2452DD46E186B7 CRC64;

Query Match 30.4%; Score 448.5; DB 11; Length 1651;
Best Local Similarity 42.2%; Pred. No. 6.7e-30;
Matches 92; Conservative 31; Mismatches 86; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDQLFGQPGPARMSCRAGSQPPPTIRWLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPRIVEHPDLIVSKGEPATLNCRAEGRPTTIEWYKGERVETDKDPRSHRMLLP 123

Qy 58 DGTLLILLOPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGRLSVAVLREDFOIQPR 117
Db 124 SGSLFFLR-----IVHGRKSRPDEGYTCVARNYLGEAVSHNASLEVAVLDRDFRQNP 177

Qy 118 DMVAVGGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHVTSGGSLLMARAEKSDXT 177
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Db 178 DMVAVGEPVMEQPRGHEPTISWKQSGPLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSQEQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 275

RESULT 7
QY96N7 PRELIMINARY; PRT; 1651 AA.
AC QY96N7;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Roundabout 1.
GN ROBO1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBT_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98117249; PubMed=9458045;
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.;
RT "Roundabout controls axon crossing of the CNS midline and defines a
RT novel subfamily of evolutionarily conserved guidance receptors.";
RL Cell 92:205-215(1998).
DR EMBL; AF040990; AAC39575.1; -.
DR HSP; P56276; 1TLK.
DR Genew; HGNC:10249; ROBO1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
SQ SEQUENCE 1651 AA; 180929 MW; 9D98CD7CAB73074D CRC64;

Query Match 30.3%; Score 446.5; DB 4; Length 1651;
Best Local Similarity 41.7%; Pred. No. 1e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDLQFQGPGRMCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIEWYKGERVETDKDPRSHRMLP 123
Qy 58 DGTLLQLPPARGHAHQALSTDLGVYTCASNRLGTAVSRGRLSVAVLRDFQIQPR 117
Db 124 SGLFFLR-----IVHGKSRPDEGVYVCVARNYLGEAVSHNASLEVAIRLDDFRQNP 177
Qy 118 DMVAVGEQFTLECGPPKGPHEPTVSWKDGKPLALQGRHTVSGSLLMARAKSDEXT 177
Db 178 DMVAVGEPVMEQPRGHEPTISWKQSGPLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSQEQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 275

Query Match 30.3%; Score 446.5; DB 4; Length 1651;
Best Local Similarity 41.7%; Pred. No. 1e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDLQFQGPGRMCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIEWYKGERVETDKDPRSHRMLP 123
Qy 58 DGTLLQLPPARGHAHQALSTDLGVYTCASNRLGTAVSRGRLSVAVLRDFQIQPR 117
Db 124 SGLFFLR-----IVHGKSRPDEGVYVCVARNYLGEAVSHNASLEVAIRLDDFRQNP 177
Qy 118 DMVAVGEQFTLECGPPKGPHEPTVSWKDGKPLALQGRHTVSGSLLMARAKSDEXT 177
Db 178 DMVAVGEPVMEQPRGHEPTISWKQSGPLDDKDERITIRGGKLMITYTRKSDAGK 237
Qy 178 YMCVATNSAGHRESRAARVSQEQDYTEPVELLAVRI 215
Db 238 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 275

RESULT 8
O89026 PRELIMINARY; PRT; 1612 AA.
AC O89026;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Dutt1 protein.
GN ROBO1 OR DUT11.
```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Wu M.C., Lowe N., Fordham R., Rabbitts P.;
RT "The mouse homologue of human DUT11/H-robo1 gene: protein sequence and
RT chromosomal location.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17793; CAA76850.1; -.
DR HSP; P56276; 1TLK.
DR MGD; MGI:1274781; Robo1.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
SQ SEQUENCE 1612 AA; 176406 MW; 5F2988C544796B4B CRC64;

Query Match 30.2%; Score 445.5; DB 11; Length 1612;
Best Local Similarity 41.7%; Pred. No. 1.2e-29;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPQDLQFQGPGRMCRASQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 25 EDFPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIEWYKGERVETDKDPRSHRMLP 84
Qy 58 DGTLLQLPPARGHAHQALSTDLGVYTCASNRLGTAVSRGRLSVAVLRDFQIQPR 117
Db 85 SGLFFLR-----IVHGKSRPDEGVYVCVARNYLGEAVSHNASLEVAIRLDDFRQNP 138
Qy 118 DMVAVGEQFTLECGPPKGPHEPTVSWKDGKPLALQGRHTVSGSLLMARAKSDEXT 177
Db 139 DMVAVGEPVMEQPRGHEPTISWKQSGPLDDKDERITIRGGKLMITYTRKSDAGK 198
Qy 178 YMCVATNSAGHRESRAARVSQEQDYTEPVELLAVRI 215
Db 199 YVCVGTNNVGERSEVAVELTVLERPSFVKRPSNLAVTV 236

RESULT 9
QY0242 PRELIMINARY; PRT; 330 AA.
AC QY0242;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Roundabout1 protein (fragment).
GN ROBO1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBT_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21366016; PubMed=11472852;
RA Vargesson N., Luria V., Messina I., Erskine L., Laufer E.;
RT "Expression patterns of Slit and Robo family members during vertebrate
RT limb development.";
RL Mech. Dev. 106:175-180(2001).
DR EMBL; AF364047; AAK94293.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 3.
```



DR PROSITE; PS50835; IG LIKE; 3.  
KW Immunoglobulin domain.  
FT NON\_TER 1  
FT NON\_TER 330 330  
SQ SEQUENCE 330 AA; 36725 MW; 061348878CEBE61 CRC64;  
  
Query Match 30.0%; Score 442.5; DB 13; Length 330;  
Best Local Similarity 41.3%; Pred. No. 3.1e-30;  
Matches 90; Conservative 32; Mismatches 87; Indels 9; Gaps 2;  
  
QY 1 QDSPQILVHPQDQLFQGGPGPARMSCRAGQPPTIRMLNGQPLSMVPPDPHH---LLP 57  
DB 19 EDFPPRIIVEHPSDLIVSGEPATLNCKAEGRPPTIWKYKGERVETDKDDPSRHRMLLP 78  
QY 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGALRSVAVLRDFOIQPR 117  
DB 79 SGLSFLFLR-----IVHGKSRPDGCVVVCARNYLGEAVSNASLEVALLRDFFRQNP 132  
QY 118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPRHTVSGSLLMARAESDXT 177  
DB 133 DMVAVGEPVAMECQPPRGHPPTISWKKDGTFLDDKDERITIRGKLMITVTRKNDAGK 192  
QY 178 YMCVATNSAGHRESRAARVSIOEQPDYTEPEVELLAVRI 215  
DB 193 YVCVGTNMVGERSEVAELTVLERPSFVKRPSNLAATV 230

## RESULT 10

Q8UVD7 PRELIMINARY; PRT; 1614 AA.  
AC Q8UVD7;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Roundabout-1.  
GN ROBO1.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Connor R.M., Key B.;  
RT "Dual role for Roundabout-1 in neural differentiation and axon  
pathfinding in the Xenopus forebrain."  
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF461119; AAL66361.1; -  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_C2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; ig; 5.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00408; IGC2; 5.  
DR PROSITE; PS50835; IG LIKE; 5.  
KW Immunoglobulin domain.  
SQ SEQUENCE 1614 AA; 176733 MW; 01D2C3D6593F3935 CRC64;

Query Match 29.3%; Score 432; DB 13; Length 1614;  
Best Local Similarity 40.6%; Pred. No. 1.7e-28;  
Matches 89; Conservative 32; Mismatches 88; Indels 10; Gaps 3;

QY 1 QDSPQILVHPQDQLFQGGPGPARMSCRAGQPPTIRMLNGQPLSMVPPDPHH---LLP 57  
DB 26 EDFPPKIVEHPSDLIVSGEPATLNCKAEGRPPTIWKYKGERVETDKDDPSRHRMLLP 85  
QY 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGALRSVAVLRDFOIQPR 117  
DB 86 SGLSFLFLR-----IVHGKIRPDGCVVVCARNYLGEAVSNASLEVALLRDFFRQNP 139  
QY 118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPL-ALQPRHTVSGSLLMARAESDEX 176

DB 140 DMVAVGEPVAMECQPPRGHPPTISWKKDGTFLDDKDERITIRGKLMITYTRKSDAG 199  
QY 177 YMCVATNSAGHRESRAARVSIOEQPDYTEPEVELLAVRI 215  
DB 200 KYVCVGTNMVGERSEVAELTVLERPSFLRRPSNNAATV 238  
  
RESULT 11  
Q90Z70 PRELIMINARY; PRT; 1513 AA.  
AC Q90Z70;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Roundabout2.  
GN ROBO2.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21270059; PubMed=11376489;  
RA Lee J.S., Ray R., Chien C.B.;  
RT "Cloning and expression of three zebrafish roundabout homologs suggest  
RT roles in axon guidance and cell migration."  
RL Dev. Dyn. 221:216-230(2001).  
DR EMBL; AF337035; AAK58427.1; -  
DR ZFIN; ZDB-GENE-001019-1; robo2.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_C2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; ig; 5.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00408; IGC2; 5.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
KW Immunoglobulin domain.  
SQ SEQUENCE 1513 AA; 165181 MW; D1743BACCC089F0 CRC64;

Query Match 28.5%; Score 420.5; DB 13; Length 1513;  
Best Local Similarity 36.4%; Pred. No. 1.6e-27;  
Matches 92; Conservative 38; Mismatches 92; Indels 31; Gaps 6;

QY 1 QDSPQILVHPQDQLFQGGPGPARMSCRAGQPPTIRMLNGQPLSMVPPDPHH---LLP 57  
DB 26 EDFPPRIIVEHPSDLIVSGEPATLNCKAEGRPPTIWKYKGERVETDKDDPSRHRMLLP 85  
QY 58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGALRSVAVLRDFOIQPR 117  
DB 86 SGLSFLFLR-----IVHGKSRKPDEGAVVCARNYLGEAVSNASLEVALLRDFFRQNP 139  
QY 118 DMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPRHTVSGSLLMARAESDXT 177  
DB 140 DMVAVGEPVAMECQPPRGHPPTISWKKDGTFLDDKDERITIRGKLMISNTRKSDAG 199  
QY 178 YMCVATNSAGHRESRAARVSI-QSPQDYTEPV-----ELLAVRIQLENVTLNPPDAE 229  
DB 200 YICVGTNMVGERSEVAELTVLERPSFLRRPTNQLVLEEAVERFCVQV-----DPQPS- 254  
QY 230 GPKPRPAVLXWK 242  
DB 255 -----IRWK 258  
  
RESULT 12  
Q9Z214 PRELIMINARY; PRT; 1344 AA.  
ID Q9Z214



[illegible]

Search completed: January 30, 2004, 15:56:29  
Job time : 30.0777 secs

	Query Match	27.2%;	Score 401.5;	DB 13;	Length 1389;
	Best Local Similarity	36.7%;	Pred. No. 6.3e-26;		
	Matches	92;	Conservative 36;	Mismatches 26;	Indels 27; Gaps 6
Qy	1	QDSPPGILVHPQDQLFOGFGPARMSCRASGOPPTIRWLLNGOPLSMVPPDPHH---	LLP	57	
	.				
Db	28	EDAAPRIVEHSDLVSGEPAITCKAEGRTPMVEYKDGSRVETDREDPSHRMLLP		87	
Qy	58	DGTLALLQPPARGHAHQDQALSTDLGVYTCASNRLGTAVSGARLSAVILREDFOIQRP		117	

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:45:39 ; Search time 9.53368 Seconds  
(without alignments)  
1361.423 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303  
Perfect score: 1475  
Sequence: 1 QDSPPQLVHPDQLFQPGF.....SGPRLPREARELRGQRNTG 276

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	232.5	15.8	1997	PTPF HUMAN
2	230.5	15.6	1040	AXOI_RAT
3	228	15.5	1040	AXOI_HUMAN
4	225	15.3	3707	PGSM_MOUSE
5	222	15.1	1912	PTPD_HUMAN
6	222	15.1	2029	LAR_DROME
7	221.5	15.0	1377	NEOI_RAT
8	215.5	14.6	1443	NEOI_CHICK
9	214.5	14.5	1461	NEOI_HUMAN
10	213.5	14.5	1036	AXOI_CHICK
11	212.5	14.4	1070	PTK7_HUMAN
12	209	14.2	1447	DCC_MOUSE
13	209	14.2	1493	NEOI_MOUSE
14	206	14.0	1447	DCC_HUMAN
15	203.5	13.8	4391	PGSM_HUMAN
16	202	13.7	837	NCM2_MOUSE
17	199.5	13.5	1302	NRG_DROME
18	195.5	13.3	1091	NCAL_CHICK
19	195.5	13.3	6632	UN99_CABEL
20	194.5	13.2	1284	NRCA_CHICK
21	193	13.1	837	NCM2_HUMAN
22	191.5	13.0	1914	KML5_HUMAN
23	191	12.9	1260	CAML_MOUSE
24	186	12.6	416	RAGE_BOVIN
25	185	12.5	725	NC42_MOUSE
26	185	12.5	1115	NC41_MOUSE
27	185	12.5	1257	CAML_HUMAN
28	184	12.5	1051	PTK7_CHICK
29	183	12.4	858	NC41_RAT
30	182.5	12.4	1010	CONT_CHICK
31	182	12.3	1259	CAML_RAT
32	181.5	12.3	333	AMAL_DROME
33	181.5	12.3	3375	UN52_CABEL

34	179	12.1	2012	1	DSCA_HUMAN
35	176	11.9	853	1	NCAL_BOVIN
36	176	11.9	2200	1	LAR_CABEL
37	175	11.9	1266	1	NGCA_CHICK
38	174.5	11.8	873	1	FAS2_DROME
39	173.5	11.8	761	1	NC42_HUMAN
40	173.5	11.8	848	1	NC41_HUMAN
41	172	11.7	404	1	RAGE_HUMAN
42	170.5	11.6	1018	1	CONT_HUMAN
43	168	11.4	1021	1	CONT_RAT
44	167.5	11.4	912	1	IC45_RABIT
45	165.5	11.2	1020	1	CONT_MOUSE

ALIGNMENTS

RESULT 1

ID	PTPF HUMAN	STANDARD	PRT	1897 AA
AC	P10586;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	LAR protein precursor (leukocyte antigen related) (EC 3.1.3.48)			
GN	PTPRF OR LAR			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Tonsil;			
EX	MEDLINE=89035978; PubMed=2972792;			
RA	Streuli M., Krueger N.X., Hall L.R., Schloeman S.P., Saito H.;			
RT	"A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte common antigen.";			
RL	J. Exp. Med. 168:1523-1530(1988).			
RN	[2]			
RP	MUTAGENESIS			
EX	MEDLINE=90046860; PubMed=2554325;			
RA	Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;			
RT	"A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).			
RN	[3]			
RP	MUTAGENESIS			
EX	MEDLINE=90316093; PubMed=1695146;			
RA	Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;			
RT	"Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and LAR.";			
RL	EMBO J. 9:2399-2407(1990).			
CC	-!- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR. IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASE).			
CC	-!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY. WHILE THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE FIRST ONE.			
CC	-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.			
CC	-!- SIMILARITY: Contains 8 fibronectin type III domains.			
CC	-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			









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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
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; PRIOR APPLICATION NUMBER: 60/082569  
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; PRIOR APPLICATION NUMBER: 60/082704  
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; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
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; PRIOR FILING DATE: 1998-04-22  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
  
Query Match 88.9%; Score 1311; DB 11; Length 985;  
Best Local Similarity 98.8%; Pred. No. 3.7e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
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Db 6 QDSPQILVHPQDQLFQGGPGPARMSCQASGQPPPTIRWLLNGQLPSMWVPPDPHLLPDGT 65  
  
Qy 61 LLLLQPPARGHADGQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLRDEFQIQPRDMV 120  
Db 66 LLLLQPPARGHADGQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLRDEFQIQPRDMV 125  
  
Qy 121 AVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPRHTVSGSLLMARAEKSDEXTVMC 180  
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Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240  
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Qy 241 WKVSGP 246  
Db 246 WKVSGP 251

RESULT 12  
US-09-978-403A-211  
; Sequence 211, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gevirtzen, Mary E.  
; APPLICANT: Goddard, Audrey  
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; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C17

; CURRENT APPLICATION NUMBER: US/09/978,403A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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Query Match      88.9%; Score 1311; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 121 AVVGEQFTLECPGPHGPEPTVSWWKGKPLAQPGRTVSGSLLMARAESDSEXTYMC 180
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Qy 241 WKVSGP 246
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; Sequence 211, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Sheiton, David L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC25
; CURRENT APPLICATION NUMBER: US/09/978.564A
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 11; Length 985;

Best Local Similarity 98.8%; Fred. No. 3.7e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDSPPQILVHPQDLFOGPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
Db 6 QDSPPQILVHPQDLFOGPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 65  
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Qy 121 AVVGEQFTLECGPPWGHPEPTVSNWKGKPLALQPGRHTVSGSLLMARAEKSDGYTMC 180  
Db 126 AVVGEQFTLECGPPWGHPEPTVSNWKGKPLALQPGRHTVSGSLLMARAEKSDGYTMC 185  
Qy 181 VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENVTLLNPDPAEGPKRPVWLX 240  
Db 186 VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENVTLLNPDPAEGPKRPVWLX 245  
Qy 241 WKVSGP 246  
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RESULT 14

US-09-999-833A-211  
; Sequence 211, Application US/09999833A  
; Publication No. US20030054405A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
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APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
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APPLICANT: Tumaas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC65  
CURRENT APPLICATION NUMBER: US/09/999,833A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C12  
CURRENT APPLICATION NUMBER: US/09/981.915A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728

Query Match 88.9%; Score 1311; DB 11; Length 985;  
Best Local Similarity 98.8%; Pred. No. 3.7e-100; Indels 0; Gaps 0;  
Matches 243; Conservative 1; Mismatches 2;  
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Db 6 QDSPPQILVHPDQDLFQCGPGPARMSCRASGQPPPTIRLLNGQPLSMVPPDPHLLPDGT 65  
Qy 61 LLLLOPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFOIQRDMV 120  
Db 66 LLLLOPPARGHAHDGQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFOIQRDMV 125  
Qy 121 AVVGEQFTLECGPWHGHEPTVSWKDGKPLALQGRHTVSGSLLMARAKSDEXTVMC 180  
Db 126 AVVGEQFTLECGPWHGHEPTVSWKDGKPLALQGRHTVSGSLLMARAKSDEXTVMC 185  
Qy 181 VATNSAGHRESRAARVSIQEQDYTPVELLAVRIQLENVTLNPDPAEGPKRPVWLX 240  
Db 186 VATNSAGHRESRAARVSIQEQDYTPVELLAVRIQLENVTLNPDPAEGPKRPVWLX 245  
Qy 241 WKVSGP 246  
Db 246 WKVSGP 251

RESULT 15  
US-09-981-915A-211  
; Sequence 211, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:

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;; PRIOR APPLICATION NUMBER: 60/079786  
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Query Match 88.9%; Score 1311; DB 11; Length 985;

Best Local Similarity 98.8%; Pred. No. 3.7e-100;

Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRLLNGQPLSMVPPDPHLLPDGT 60

Db 6 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRLLNGQPLSMVPPDPHLLPDGT 65

Qy 61 LLLQLPPARGHADQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDEFQIQPRDMV 120

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Qy 121 AVVGEQFTLEGCPWGHPEPTVSWWKDKPLALQGRITVSGGSLLMARAESDXTYMC 180

Db 126 AVVGEQFTLEGCPWGHPEPTVSWWKDKPLALQGRITVSGGSLLMARAESDXTYMC 185

Qy 181 VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENVTLINPDPAEGKPRPAVWLX 240

Db 186 VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENVTLINPDPAEGKPRPAVWLX 245

Qy 241 WKVSGP 246

Db 246 WKVSGP 251  
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Search completed: January 30, 2004, 15:59:03  
Job time : 29.1244 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2004, 11:38:39 ; Search time 2894.42 Seconds  
(without alignments)  
3900.967 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303  
Perfect score: 1475  
Sequence: 1 QDSPPQILVHPDQLFQPG.....SGPRLPREARELRGRRNTG 276

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-Q/cgn2\_1/USPTO\_spool\_p/US10047021/runat\_30012004\_145452\_24562/app.query.fasta\_1.910  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10047021@cgn 1 1 5066 @runat\_30012004\_145452\_24562 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: 1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.tv.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

29: em.vl.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rod.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.av.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1469	99.6	1346	6	BD074325 50 human
2	1432	97.1	3267	6	AX405719 Sequence
3	1432	97.1	3872	9	AF361473 Homo sapi
4	1424	96.5	4262	6	BD012213 Homo sapi
5	1424	96.5	4262	6	BD160172 Primer fo
6	1424	96.5	4262	9	AK027852 Homo sapi
c 7	1232.5	83.6	186971	9	AP003501 Homo sapi
8	1121	76.0	3467	9	BC014995 Homo sapi
9	1061.5	72.0	2886	10	AY277635 Rattus no
10	1057	71.7	756	6	BD150226 Primer fo
11	869	58.9	4694	9	AK074163 Homo sapi
12	827.5	56.1	209012	2	AC105958 Mus muscu
c 13	827.5	56.1	214559	2	AC138284 Mus muscu
c 14	795.5	53.9	223269	2	AC120636 Rattus no
15	795.5	53.9	250318	2	AC109983 Rattus no
16	450.5	30.5	4956	10	AF041082 Rattus no
17	448.5	30.4	3384	6	AX714308 Sequence
18	448.5	30.4	3384	9	AK056544 Homo sapi
19	447.5	30.3	6922	10	MMU17793 Y17793 Mus musculu
20	446.5	30.3	4956	6	BD085989 Method of
21	446.5	30.3	4956	9	AF040990 Homo sapi
22	446.5	30.3	6789	9	HSDUT1 295705 Human DNA
23	442.5	30.0	991	5	AF364047 Gallus ga
24	432	28.3	6435	5	AF461119 Xenopus l
25	423	28.7	4871	5	AF337035 Danio rer
26	414.5	28.1	5259	10	AF060570 Mus muscu
27	404.5	27.4	5598	9	AB046788 Homo sapi
28	404.5	27.4	6215	6	AX556709 Sequence
29	403.5	27.4	1565	5	AF364048 Gallus ga
30	401.5	27.2	5067	5	AF304131 Danio rer
31	401.5	27.2	5384	5	AF337036 Danio rer
32	400.5	27.2	6860	5	AF304130 Danio rer
33	396.5	26.9	6445	6	AX556703 Sequence
34	395.5	26.8	4188	6	BD085986 Method of
35	395.5	26.8	6440	3	AF040989 Drosophil
36	394	26.7	4306	3	AF312580 Drosophil
37	354.5	24.0	3822	3	AF041053 Caenorhab
38	354.5	24.0	3894	6	BD085988 Method of
39	348.5	23.6	1129	5	AF337034 Danio rer
40	346	23.5	3650	10	AF182037 Rattus no
41	345	23.4	4146	6	BD085987 Method of
42	340	23.1	5381	3	AF312579 Drosophil
43	299.5	20.3	186971	9	AP003501 Homo sapi
c 44	292.5	19.8	16652	2	AC014298 Drosophil
c 45	292.5	19.8	169534	3	AC008350 Drosophil

ALIGNMENTS

RESULT 1

BD074325  
LOCUS BD074325 1346 bp DNA linear PAT 27-AUG-2002  
DEFINITION 50 human secreted proteins.  
ACCESSION BD074325  
VERSION BD074325.1 GI:22619928  
KEYWORDS JP 2001514024-A/30.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1346)  
AUTHORS Moore,P.A., Ruben,S.M., Lafleur,D.W., Shi,Y., Rosen,C.A.,  
Olson,H.S., Ebner,R. and Brewer,L.A.  
TITLE 50 human secreted proteins  
JOURNAL Patent: JP 2001514024-A 30 11-SEP-2001;  
HUMAN GENOME SCIENCES INC  
COMMENT OS Homo sapiens (human)  
PN JP 2001514024-A/30  
PD 11-SEP-2001  
PF 03-SEP-1998 JP 2000508394  
PR 05-SEP-1997 US 60/057626 05-SEP-1997 US 60/057663 PR  
05-SEP-1997 US 60/057669,12-SEP-1997 US 60/058667 PR  
12-SEP-1997 US 60/058974,12-SEP-1997 US 60/058973 PR  
12-SEP-1997 US 60/058666  
PI PAUL A MOORE, STEVEN M RUBEN, DAVID W LAFLEUR, YANGGU SHI, CRAIG A  
ROSEN  
PI HENRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER PC  
C12N15/09,A61K38/00,A61K48/00,A61P17/02,A61P17/06,A61P19/00, PC  
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PC C12N1/15,  
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LOCUS AX405719  
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ACCESSION AX405719  
VERSION AX405719.1 GI:21438877  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,  
Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.  
TITLE Novel nucleic acids and polypeptides  
JOURNAL Patent: WO 0222860-A 134 21-MAR-2002;  
HYSEQ, INC. (US)  
FEATURES  
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Location/Qualifiers  
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ORIGIN

Alignment Scores:  
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|||||  
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DEFINITION AF361473  
ACCESSION AF361473  
VERSION AF361473.1 GI:16930357  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3872)  
AUTHORS Huminiacki, L. and Bicknell, R.  
TITLE In silico cloning of novel endothelial-specific genes  
JOURNAL Genome Res. 10 (11), 1796-1806 (2000)  
MEDLINE 20530916  
PUBMED 11076864  
REFERENCE 2 (bases 1 to 3872)  
AUTHORS Huminiacki, L. and Bicknell, R.  
TITLE Direct Submission  
JOURNAL Submitted (15-MAR-2001) ICRF, Institute of Molecular Medicine, John  
Radcliffe Hospital, Oxford OX3 9DS, UK  
FEATURES  
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ORIGIN

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## RESULT 4

BD012213 LOCUS BD012213 4262 bp DNA linear PAT 02-AUG-2002  
 DEFINITION Novel genes encoding protein kinase or protein phosphatase.

ACCESSION BD012213

VERSION BD012213.1 GI:22092402

KEYWORDS WO 0109345-A/11.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4262)

REFERENCE Ota,T., Isegai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,

Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.,

Funahashi,S., Seno,C. and Nezu,J.  
 Novel genes encoding protein kinase or protein phosphatase  
 Patent: WO 0109345-A 11 08-FEB-2001.

HELIIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,  
 KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU  
 SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, TSUKI, SHINICHI  
 FUNAHASHI, HIAMI SENO, JUNICHI NEZU

## COMMENT

OS Homo sapiens (human)  
 PN WO 0109345-A/11  
 PD 08-FEB-2001  
 PF 28-JUL-2000 WO 2000JP005060  
 PR 29-JUL-1999 JP 99P 248036, 11-JAN-2000 JP 00P 118776 PR  
 02-MAY-2000 JP 00P 183767, 18-OCT-1999 US 60/159590 PR  
 17-FEB-2000 US 60/183322  
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI  
 KAORU SAITO,  
 JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
 KEIICHI NAGAI, TETSUJI OTSUKI, SHINICHI FUNAHASHI, CHIYAKI SENO,  
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 PC C12N15/54, C12N15/55, C12N9/12, C12N9/16, C12N5/10, C12N1/21 PC  
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 Query Match: 96.54% Indels: 1  
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 Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
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Db 901 ACTGCCCGGGAGGCCAGGAGCTCCGTGGGAGAGG 937

## RESULT 5

BD160172 4262 bp DNA linear -PAT 17-JAN-2003  
LOCUS Primer for synthesizing full-length cDNA and use thereof.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS

PN

PD

PF

PI

PI

PI

PC

C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC

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PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH key

Location/Qualifiers

(40).. (2415).

FT CDS

Location/Qualifiers

1..4262

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BASE COUNT 873 a 1333 c 1209 g 847 t

ORIGIN

Alignment Scores:

Pred. No.: 3 246-75 Length: 4262

Score: 1424.00 Matches: 267

Percent Similarity: 98.11% Conservative: 1

Best local Similarity: 97.80% Mismatches: 4

Query Match: 96.54% Indels: 1

DB: 6 Gaps: 0

US-10-047-021-86\_copy\_28\_303 (1-276) x BD160172 (1-4262)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnClnGlyProGly 20

Db 121 CAGGACTCCCCGCCCCAGATCTCTAGTCCACCCCAAGGACCACTGTTCAGGGGCCCTGGC 180

Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTyrLeuLeu 40

Db 181 CCTGCCAGATGAGCTGCAAGCCTCAGCCAGCCACCTCCACCATCCGCTGTGTCTG 240

Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60

Db 241 AATGGCAGCCCTGAGCATGTGTCGCCCAAGCCACACCACTCTCTGCTGATGGGACC 300

Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80

Db 301 CTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACAGATGGCCAGCCCTGTCCACA 360

Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100

Db 361 GACCTGGGTGCTACACATGTGAGCCAGCAACCGGCTTGGCACCGCAGTCAGCAGAGGC 420

Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120

Db 421 GCTGGCTGTCTGTGGCTGCTCTCCGGGAGGATTTCCAGATCCAGCTCGAGACATGGTG 480

Qy 121 AlaValValGlyGluGlnPheThrLeuGlnCysGlyProProTyrProTyrGlyHisProGluPro 140

Db 481 GCTGGTGGGTGAGCAGTCTTACTCTGGAATGTGGCGCGCCCTGGGGGCCACCCAGAGCCC 540

Qy 141 ThrValSerTyrTyrLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160

Db 541 ACAGTCTCATGTGGAAAGATGAGAAACCCCTGGCCCTCCAGCCCGGAGGCACACAGTG 600

Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*ThrTyrMetCys 180

Db 601 TCCGGGGGGTCCCTGCTGATGGCAAGACAGACAGAGAGTGCAGAGGACCTTACATGTGT 660

Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200

Db 661 GTGGCCACCAACAGCGCAGGACACAGGAGAGCCCGCAGCCCGGGTTCATCCAGGAG 720

Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluVal 220

Db 721 CCCAGGACTACAGGAGCCTGTGAGCTTCTGGCTGTGCGAATTCAGCTGGAATATGTG 780

Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProAspProAlaValTyrLeu\*\* 240

Db 781 ACACCTGCTGAACCCGATCTCTCAGAGGCCCCCAAGCCTAGACCCGGGTGTGGCTCAGC 840

Qy 241 TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260

Db 841 TGGAAAGGTCAGTGGCCCTGCTGCGCTGCCCCAATCTTACACGGCTTGTTCAGGACCCAG 900

Qy 260 gluProArgGluAlaArgGluLeuArgGlyClnArg 272

Db 901 ACTGCCCGGGAGGCCAGGAGCTCCGTGGGAGAGG 937

## RESULT 6

AK027852

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AK027852 4262 bp mRNA linear PRI 01-AUG-2002

Homo sapiens cDNA FLJ14946 fis, clone PLACE2000034, weakly similar

to LAR PROTEIN PRECURSOR (EC 3.1.3.48).

AK027852

AK027852.1 GI:14042831

oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, Y.,

Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., and Oshina, A.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 4262)  
Isogai, T. and Otsuki, T.  
Direct Submission  
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1332-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

## FEATURES

Location/Qualifiers

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/db\_xref="taxon:9606"  
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## BASE COUNT

873 a 1333 c 1209 g 847 t

## Alignment Scores:

Pred. No.: 3.24e-75 Length: 4262  
Score: 1424.00 Matches: 267  
Percent Similarity: 98.17% Conservative: 1  
Best Local Similarity: 97.80% Mismatches: 4  
Query Match: 96.54% Indels: 1  
DB: 9 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x AK027852 (1-4262)

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Dy 121 CAGACTCCCCCGCCAGATCTTAGTCCACCCCGAGACAGCTGTTCCAGGGCCCTGGC 180  
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
Dy 181 CCTGCCAGGATGAGTGCAGACCTCAGGCAGCCACCTCCACCATCCGCTGGTGTG 240  
Qy 41 AsnGlyGlnProLeuSerMetValProAspProHisHisLeuLeuProAspGlyThr 60  
Dy 241 AATGGGAGCCCTGAGCATGGTGGCCCGACACACACACCTCCCTGCTGATGGGACC 300  
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80

Db 301 CTTCCTGCTGTACAGCCCCCTGCCCGGGGACATGCCACCATGGCCAGGCGCTGTCCACA 360  
Qy 81 AspleuclyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Dy 361 GACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTTGGCAGCGGAGTCCAGAGGC 420  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Dy 421 GCTCGGCTGTCTGGGCTGTCTCCGGGAGGATTTCCAGATCCAGCTCCGAGACATGGT 480  
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140  
Dy 481 GCTGTGGTGGTGGAGGATTTACTCTGGAATGTGGGCGGCCCTCCAGAGAGCC 540  
Qy 141 ThrValSerTrpTrpTyAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160  
Dy 541 ACAGTCTCATGGTGGGAAGATGAGAAACCCCTGGCCCTCCAGCCCGGAAGGACACAGT 600  
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyMetCys 180  
Dy 601 TCCGGGGGGTCCCTGCTGATGGCAAGACAGAGAGTGCAGAGGACCTACATGTGT 660  
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
Dy 661 GTGGCCACCAACAGCGCAGGACACAGGAGAGCGCGGCGGCTTCCATCCAGGAG 720  
Qy 201 ProGlnAspTyThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220  
Dy 721 CCCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTGGCAATTCAGCTGGAAAAATGT 780  
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\* 240  
Dy 781 ACATGCTGAACCCGGATCTCTGACAGGGGCCCCAGCCTAGACCGCGGTGTGCTCAGC 840  
Qy 241 TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260  
Dy 841 TGAAGGTCAAGTGGCCCTGCTGGCGCTGCCCAATCTTACACGGCGCTTGTTCAGGACC 900  
Qy 260 gLeuProArgGluAlaArgLeuLeuArgGlyGlnArg 272  
Dy 901 ACTGCCCCGGAGGCCAGGAGCTCCGTGGGCGAGAG 937  
RESULT 7  
AP003501/c 186971 bp DNA linear PRI 08-MAR-2002  
LOCUS Homo sapiens genomic DNA, chromosome 11q, clone:RP11-664I21,  
DEFINITION complete sequence.  
ACCESSION AP003501  
VERSION AP003501.2 GI:19263048  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Homo sapiens  
Bukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Homo sapiens genomic DNA  
Published Only in Database (2001)  
2 (bases 1 to 186971)  
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (11-APR-2001) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
On Mar 7, 2002 this sequence version replaced gi:13603460.  
COMMENT  
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Location/Qualifiers  
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BASE COUNT 49646 a 38908 c 40035 g 58382 t  
ORIGIN

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Score: 1232.50 Matches: 267  
Percent Similarity: 48.46% Conservative: 1  
Best Local Similarity: 48.28% Mismatches: 4  
Query Match: 83.56% Indels: 282  
DB: Gaps: 4

US-10-047-021-86\_COPY\_28\_303 (1-276) x AP003501 (1-186971)

QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
DB 32330 CAGGACTCCCGCCCGCAGATCCTAGTCCACCCCGCAGGACAGCTGTTCCAGGCGCCCTGGC 32271  
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
DB 32270 CCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCAGCCACCTCCACCATCCGCTGGTGTG 32211  
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisLeuLeuProAspGlyThr 60  
DB 32210 AATGGCAGCCCTGAGCATGTGTCGCCCGCAGCCACACACCACTCTGCTGATGGGACC 32151  
QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
DB 32150 CTTCTGCTGCTACAGCCCTGCGCGGGACATGCCACGATGGCCAGGCGCCCTGTCCACA 32091  
QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
DB 32090 GACCTGGGTGTCTACACATGTGAGGCGCAGCAACCGGCTTGGCAGCGCAGCTCAGCAGAGGC 32031  
QY 101 AlaArgLeuSerValAla----- 106  
DB 32030 GTCGGCTGTCTGTGGCTGTGAGGCTGGAGGGGAGGCTTCAGGGTGGGGCAACCTGG 31971  
QY 106 ----- 106  
DB 31970 GTGGAGACATCTGAGCTGAATGTTCAAGGGAACATCTGAGAGGTGAGTGGGATCCTGTG 31911  
QY 106 ----- 106  
DB 31910 AGCAGAGGCTGGGCTGGAAGGCTTGGGAGGGCAAGCTGGGGGGGCTGGCCCTAAATG 31851  
QY 106 ----- 106  
DB 31850 GGAGGCCAGAGGTGGGCAAGCAGAGAGGGGCAAGAGTGTATAGGGAGAGAGAGAGG 31791  
QY 107 -----ValLeuArgGluAspPheGln 113  
DB 31790 CTTGGGCCCTGCTCCGTGTACCTTCCATCCTCCCCACAGTCTCTCCGGGAGGATTTCCAG 31731  
QY 114 IleGlnProArgAspMetValAlaValAlaValGlyGlnPheThrLeuGluCysGlyPro 133  
DB 31730 ATCCAGCCTCGGACATGTGGCTGTGGTGGGTGAGCAGTCTTACTCTGGAATGTGGGCGC 31671  
QY 134 ProTrpGlyHisProGlnProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 153  
DB 31670 CCTGGGGGCCACCCAGAGCCACAGTCTCATGTGTGAAGATGGGAACCCCTGGCCCTC 31611  
QY 154 GlnProGlyArgHisThrVal----- 160  
DB 31610 CAGCCCGGAAGGCACACAGT-AAGTGTGGCCCTCCCCACACATTCATCCTGGGCTGGG 31552  
QY 160 ----- 160  
DB 31551 CAGACCTGGGTACACCTGATGGACTGACCTGCGGTCCAGCCCGCATCCTCCGCTAGAA 31492

QY 160 ----- 160  
DB 31491 TTTGAGGAGGGAGAGAGAGGGGGCCTCAAACTTCCCCCGAGCTCAGAGCCCTCCCCACA 31432  
QY 161 -----SerGlyGlySerLeuLeuMetAla 168  
DB 31431 TAGGAGACTTCACAGTGAACCTGGCCCTGACAGAGTGTCCGGGGGTCTCCCTGCTGATGGCA 31372  
QY 169 ArgAlaGluLysSerAspGly\*\*\*ThrTyrMetCysValAlaAlaThrAsnSerAlaGlyHis 188  
DB 31371 AGAGCAGAGAAGAGTGACGAAGGACCTACATGTGTGTGTGGCCACCACACAGCGCAGGACAT 31312  
QY 189 ArgGluSerArgAlaAlaArgValSerIleGln----- 199  
DB 31311 AGGGAGAGCGCGCAGCCCGGGTTTCCATCCAGGGGTAAAGGCAGGGGTGGGTACAAATCA 31252  
QY 199 ----- 199  
DB 31251 GAGCCAGGCTGCAGGCTCCAGTTGGGGTGTGTATTCTGTGTTTGGGTGGGGTTAAGGTA 31192  
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DB 31071 CCTGGCTCAGGGATGTTCCAGCCTCAGTTCGTCTGCTGTGCTATATAAGCCCGCAGCCC 31012  
QY 200 -----GluProGlnAspTyrThrGluProValGluLeuAlaVal 213  
DB 31011 AGCCCTATCTCCCCACAGAGCCCGCAGGAGTACACGGAGCTGTGGAGCTTCTGGCTGTG 30952  
QY 214 ArgIleGlnLeuGluAsnValThrLeuLeuLeuAsnProAspProAlaGluGlyProLysPro 233  
DB 30951 CGAATTACGTGGAANAATGTGACACTGTGAACCCCGGATCTTCGACAGAGGGCCCGCAGCCT 30892  
QY 234 ArgProAlaValTrpLeu\*\*\*TrpLys----- 242  
DB 30891 AGACCGCGGTGTGGCTCAGCTGGAAGGTGAGGACAGGTGTAAAGGGTAAAGCCGATC 30832  
QY 242 ----- 242  
DB 30831 CAGAGCTCAAGAAAGGGGCTTCTGAGCTCTCTGACCCCGCCCTTCTCGAAACTCTCT 30772  
QY 243 -----ValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260  
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QY 260 gIeuProArgGluAlaArgGluLeuArgGlyGlnArg 272  
DB 30711 ACTGCCCGGGAGGCGCAGGAGCTCCGTGGGCAGAGG 30675

## RESULT 8

BC014995

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

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Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

BC014995

Homo sapiens, clone IMAGE:4850025, mRNA.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3467)

Strausberg, R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer



Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Susanna Chan, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Steven Jones, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeeidi, Jacqueline  
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IPAL Plate: 34 Row: a Column: 19.

## FEATURES

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664 t
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BASE COUNT  
ORIGIN

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Score: 1121.00 Matches: 213
Percent Similarity: 98.16% Conservative: 0
Best Local Similarity: 98.16% Mismatches: 3
Query Match: 76.00% Indels: 1
DB: 9 Gaps: 0
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US-10-047-021-86\_COPY\_28\_303 (1-276) x BC014995 (1-3467)

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Db 2 CCTGATGGGACCTTCTGCTGCTACAGCCCTGCGCGGACATGCCACGATGGCCAG 61
Qy 77 AlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAla 96
Db 62 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCGACCAACCGCTTGGCAGCGCA 121
Qy 97 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 116
Db 122 GTCAGCAGACGGCTCGGCTGTCTGTGCTGTCTCCGGGAGATTTCAGATCCAGGCT 181
Qy 117 ArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 136
Db 182 CGGACATGGTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 241
Qy 137 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 156
Db 242 CACCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA 301
Qy 157 ArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 176
Db 302 AGGCACACAGTGTCCGGGGGATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 361
Qy 177 ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 196
Db 362 ACCTACATGTGTGTGGCCACCAACAGCGCAGGACAGGAGCGCGCGCAGCGCGCGGT 421
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Qy 197 SerIleGlnGluProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleGln 216
Db 422 TCCATCCAGAGAGCCCGAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGGGATTCAG 481
Qy 217 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 236
Db 482 CTGGAAATGTGACACTGCTGACCCGATCTCTGAGAGGCGCCCAAGCCTAGACCGCGC 541
Qy 237 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys 256
Db 542 GTGTGGCTCAGCTGGAAGGTGAGTGGGCTCTGCTGGCTTGCCTTACACGCGCTTG 601
Qy 256 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 602 TTCAGGACCCAGACTGCCCCGGAGGCGAGGAGCTCCGTGGCGCAGAGG 650
RESULT 9
AY277635
LOCUS AY277635 2886 bp mRNA linear ROD 12-MAY-2003
DEFINITION Rattus norvegicus ROBO4 (Robo4) mRNA, complete cds.
ACCESSION AY277635
VERSION AY277635.1 GI:30575794
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2886)
AUTHORS Roberts,K.G. and Stewart,L.M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2003) CRT Development Laboratory, Cancer Research
Technology, Suite 23, Dominion House, 59 Bartholomew Close, London,
England EC1A 7BE, United Kingdom
FEATURES
Location/Qualifiers
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RPSGRARGPDSNVLLRLPEQVPSAPQSVTLRPGNSVFSVWAPPAENHNGFIRG
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EQWESQARDPSPKXHSWTLQRLATLRKPEVITAGVALLWLLGLGIVCIYRRRAG
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CARSHDQSCQVKLQAPSSDPLPAAPLVLNSRPSQSPQNSFLSVSPGSSNLSSES
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/notes="Region: immunoglobulin domain"
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/ note="polymorphism; results in leucine to proline amino acid change"
/ replace="c"
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/ gene="Robo4"
/ note="polymorphism"
/ replace="a"
BASE COUNT 591 a 908 c 814 g 573 t
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Alignment Scores:
Pred. No.: 5,478-54 Length: 2886
Score: 1061.50 Matches: 205
Percent Similarity: 82.78% Conservative: 21
Best Local Similarity: 75.09% Mismatches: 45
Query Match: 71.97% Indels: 2
DB: 10 Gaps: 1

US-10-047-021-86_COPY_28_303 (1-276) x AY277635 (1-2886)

QY 2 AspSerProGlnIleuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
DB 115 GATTTCCACCCAGATCTAGTTTCATCCCGAGGACCACTTTCAGGGCTCCGGCGG 174
QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 41
DB 175 GCCAAGATGAGTTGCAGAGCATCGCGCCCAACCACTTCCCACTATCCGCTGGCTGAAT 234
QY 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61
DB 235 GGGCAGCCCCCTCAGATCGCGACCCCACTTACATTCCTCCAAATCAGATGGGACCTC 294
QY 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln--AlaLeuSerThr 80
DB 295 CTGTACATCGCCCCCTTACCATCGAGCGCGCGGAGGACCAACATCTCTCAGCA 354
QY 81 AspLeuGlyValThrCysGlnAlaSerAenArgLeuGlyThrAlaValSerArgGly 100

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QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB 415 GCTAGGCTGTCTGTGGCTGTCTCTCAGGAGGACTTCGGGATCCCACTTCGGGACAGTG 474
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
DB 475 GCCGTGTGTGGCGAGAGCTTGGTTCTCGAGTGTGGTCTCCCTGGGGCTACCCAAAGCCT 534
QY 141 ThrValSerTrpTrpLysAspGlySerProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 535 TCAGTCTCTGTGGAAAGATGGGAAACCCCTGTGCTCCAGCCAGGGAAGCGCAGTG 594
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu--*ThrTyrMetCys 180
DB 595 TCTGGGATTTCTGTGATGGTGGCAAGACAGACAGAGAGATGACACGGGACCTATATGTGT 554
QY 181 ValAlaThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
DB 655 ATGGCCACCAACAATGCCGACCAACGGGAGAGTGGCGCAGCGGTGTCTATCCAGGAG 714
QY 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAenVal 220
DB 715 TCACCGGACCAACAGGAGCATCTAGAGCTTCTGGCTGTTCGAATTCAGCTGGAAAATGTG 774
QY 221 ThrLeuLeuAenProAspProAlaGluGlyProLysProArgProAlaValTrpLeu--* 240
DB 775 ACCCTGCTGAACCCAGAACCTGTAAAGCCCCCAAGCCCTGGGCCAGCTGTGTGGCTCAGC 834
QY 241 TrpLysValSerGlyPro--*ArgLeuProAenLeuThrArgProCysSerGlyProArg 260
DB 835 TGGAGGTGTAGCGGCCCTGTGTCACCTGCCAGTCATACACAGCCCTGTTCAGGGCGCAG 894
QY 260 GLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
DB 895 AGGGACCCAGGACAGGAGTCTCCATGGACAGAGG 931

RESULT 10
BD150226
LOCUS BD150226 756 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD150226
VERSION BD150226.1 GI:27855984
KEYWORDS JP 2002191363-A/5069.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 756)
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 5069 09-JUL-2002;
HELIX RESEARCH INSTITUTE
TITLE OS Homo sapiens (human)
JOURNAL PN 09-JUL-2002
COMMENT PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT source 1..756
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Location/Qualifiers
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FEATURES
source

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/db_xref="taxon:9606"
BASE COUNT 147 a 242 c 236 g 128 t 3 others
ORIGIN
Alignment Scores:
Pred. No.: 2,82e-54 Length: 756
Score: 1057.00 Matches: 205
Percent Similarity: 97.47% Conservatives: 1
Best Local Similarity: 96.70% Mismatches: 6
Query Match: 71.66% Indels: 2
DB: 6 Gaps: 0
US-10-047-021-86_COPY_28_303 (1-276) x BD150226 (1-756)
Qy 1 GlnAepSerProGlnInLeuValHisProGlnAepGlnLeuPheGlnGlyProGly 20
Db 121 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACCAAGCTGTTCCAGGGCCCTGGC 180
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThriLeArgTrpLeu 40
Db 181 CCTGCCAGAGTAGCTGCGCAAGCTTCAGCCGAGCCACCTCCACCATCCGCTGGTGGCTG 240
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 241 ANTGGCAGCCCTTGAGCATGGTGGCCCGAGCCACACCACTCTGCTGATGGGACC 300
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 301 CTCTGCTGCTACAGCCCTCGCCGGGAGCATGCCACAGTGGCCAGGCCCTGTCCACA 360
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 361 GACCTGGGTGTCTACATCATGTGAGCCAGCAACCGCTTGGCAGCGCATGTCAGAGGC 420
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnInLeuProArgAspMetVal 120
Db 421 GCTGGCTGTCTGTGGCTGTCTCCGGAGAGATTTCCAGATCCAGCTTCGAGACATGGTG 480
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
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Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 541 ACAGTCTCATGGTGAAGATGAGAAACCTCTGGCCCTCCAGCCCGGAGGACACACAGTG 600
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
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Qy 181 ValAlaThrAnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
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Qy 201 ProGlnAepTyrThrGluProValGlnLeuLeuAla 212
Db 719 CCCANGACTACAGGAACCTGTGGAACCTTTGGCT 754
RESULT 11
AK074163
LOCUS AK074163 Homo sapiens mRNA for FLJ00236 protein. linear PRI 15-FEB-2002
DEFINITION AK074163
ACCESSION AK074163
VERSION AK074163.1 GI:18676673
KEYWORDS fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
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TITLE The nucleotide sequence of a long cDNA clone isolated from human
       spleen
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 4694)
AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2002) Takahiro Nagase, Kazuea DNA Research
       Institute, Department of Human Gene Research; 1532-3, Yana,
       Kisarazu, Chiba 292-0812, Japan (E-mail:cdnaifooka@kazu.or.jp,
       URL:http://www.kazu.or.jp/NEDO, tel:81-438-52-3913,
       Fax:81-438-52-3914)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
       Economy, Trade and Industry of Japan; cDNA full insert and 5'- &
       3'-end one pass sequencing; Research Association for Biotechnology;
       cDNA library construction and clone selection; Kazusa DNA Research
       Institute.
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                     SGAPAAQSYALFRTQTAGGOGAPWAELLAGWQSAELGSLHWGQDYFEKVPSSG
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                     LGNTSLPPANNVTYVGEQTQLEIATHMPGYSYCVQAAVTGAGGEPSPVCLLLEQAME
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                     GSKNLQSPQAVFQALVAMRALGKLSSNSNELVTRLPPAPLPFPHTPTPTQSQQTQP
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BASE COUNT 987 a 1446 c 1251 g 1010 t
ORIGIN
Alignment Scores:
Pred. No.: 1.98e-42 Length: 4694
Score: 869.00 Matches: 164
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Best Local Similarity: 95.91% Mismatches: 5
Query Match: 58.92% Indels: 1
DB: 9 Gaps: 0
US-10-047-021-86_COPY_28_303 (1-276) x AK074163 (1-4694)
Qy 103 LeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaVal 122
Db 58 CTGCTCATCATGGTGCCTCCCGGAGGATTTCCAGATCCAGCTCCGGACATGGTGGCTGTG 117
Qy 123 ValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrVal 142
Db 118 GTGGGTGAGCAGTTTACTCTGGAATGTGGCGCCCTGGGGCCACCCAGAGCCACAGTC 177
Qy 143 SerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly 162
Db 178 TCATGGTGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAGGACACACAGTGTCCGGG 237
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QY 163 GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCysValala 182  
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 Db 298 ACCAAGCGCGAGGACATAGGAGAGCGCGAGCGCGCGGTTCCTCCAGAGAGCCCGCAG 357  
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 QY 243 ValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProArgLeuPr 262  
 Db 478 GTCATGGGCGCCCTGTGGCGCTGCCCAATCTTACAGCGGCTTGTTCAGGACCCAGACTGCC 537  
 QY 262 oArgGluAlaArgGluLeuArgGlyGlnArg 272  
 Db 538 CCGGAGGCGGAGGAGCTCCGTGGCGAGG 568

RESULT 12  
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 LOCUS Mus musculus clone RP24-325P4, DNA linear HTG 04-MAR-2003  
 DEFINITION Mus musculus clone RP24-325P4, WORKING DRAFT SEQUENCE, 9 unordered  
 pieces.  
 ACCESSION AC105958  
 VERSION AC105958.6 GI:28827995  
 KEYWORDS HTG; HTGS, PHASE1; HTGS DRAFT.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Birren,B., Nusbaum,C. and Lander,E.  
 Mus musculus, clone RP24-325P4  
 Unpublished  
 2 (bases 1 to 209012)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,  
 Brown,A., Camarata,J., Campolano,A., Chang,J.J., Chazaro,B.,  
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
 Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
 Ginde,S., Gord,S., Goyette,M., Graham,L., Hulme,W., Iliev,I., Johnson,R.,  
 Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,  
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,  
 Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,  
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,  
 Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,  
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,  
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosett,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,  
 Seaman,J., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Topham,K.,  
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE  
 JOURNAL  
 REFERENCE  
 3 (bases 1 to 209012)  
 Submitted (11-JAN-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
 Anderson,S., Archchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
 Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J.J., Choepel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K.,  
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,

Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,  
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
 Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,  
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
 O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
 Ruchanka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,  
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,  
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 4, 2003 this sequence version replaced gi:28201704.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L19390  
 Center clone name: 325\_P4

Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 206525 bases at least Q40  
 Consensus quality: 207512 bases at least Q30  
 Consensus quality: 207947 bases at least Q20  
 Insert size: 182000; agarose-fp  
 Insert size: 208212; sum-of-contigs  
 Quality coverage: 11.1 in Q20 bases; agarose-fp  
 Quality coverage: 9.7 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently  
 consists of 9 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 38270: contig of 38270 bp in length  
 \* 38271 38370: gap of 100 bp  
 \* 38371 39590: contig of 1220 bp in length  
 \* 39591 39690: gap of 100 bp  
 \* 39691 47174: contig of 7484 bp in length  
 \* 47175 47274: gap of 100 bp  
 \* 47275 61618: contig of 14344 bp in length  
 \* 61619 61718: gap of 100 bp  
 \* 61719 86099: contig of 24381 bp in length  
 \* 86100 86199: gap of 100 bp  
 \* 86200 112506: contig of 26307 bp in length  
 \* 112507 112606: gap of 100 bp  
 \* 112607 143181: contig of 30575 bp in length  
 \* 143182 143281: gap of 100 bp  
 \* 143282 179163: contig of 35882 bp in length  
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Best Local Similarity: 33.61% Mismatches: 43
Query Match: 56.10% Indels: 336
DB: 2 Gaps: 5

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Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuAsn 41
Db 8878 GCCAAGATGAGGTGCAGATCTCCGGCCCAACACCTCCACTATCCGCTGCTGTAAT 8937
Qy 42 GlyGlnProLeuSerMetValProProAspProHisHisAlaHisAspGlyGln--AlaLeuSerThr 61
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Qy 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln--AlaLeuSerThr 80
Db 8998 CTGTTACATCGCCCTCTGTCCAGGCGGCCACAGATGACCAACATCTCTCAGCA 9057
Qy 81 AspLeuGlyValThrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 9058 ATCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTGGGCACAGCAGTGCAGCGGGT 9117
Qy 101 AlaArgLeuSerValAla-
Db 9118 GCTAGGCTGTCTGTGGCTGGTGGAGGCTGGGAGGCTAGGCCAGGGGAGCAGAGTTAG 9177
Qy 106
Db 9178 GCTGAGATGCTGTGTCCAGGGAATACGAGATCTGTCTGTGAAGGGAGCGAGGACTG 9237
Qy 106
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Qy 153 LeuGlnProGlyArgHis-
Db 9538 CTCCAGCCAGGAGGCGCACAGTGAAGTGAACCCCAATCTCTGGGAACCTCTTTTGGCCATAC 9597
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 VERSION HTG; HTGS PHASE1; HTGS DRAFT.  
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 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Birren,B., Nusbaum,C. and Lander,E.  
 1 (bases 1 to 214559)  
 Mus musculus chromosome 9, clone RP23-356D13  
 Unpublished  
 2 (bases 1 to 214559)  
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Norman,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 214559)  
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagoopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

JOURNAL  
 COMMENT  
 Submitted (23-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 23, 2003 this sequence version replaced gi:28460994.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L28797  
 Center clone name: 356.D.13  
 ----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 213654 bases at least Q40  
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 Consensus quality: 214104 bases at least Q20  
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 Insert size: 214159; sum-of-contigs  
 Quality coverage: 10.7 in Q20 bases; agarose-fp  
 Quality coverage: 10.5 in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 5437: contig of 5437 bp in length  
 \* 5438 5537: gap of 100 bp  
 \* 5538 134170: contig of 128633 bp in length  
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 Score: 827.50 Matches: 204  
 Percent Similarity: 37.56% Conservative: 24



Best Local Similarity: 33.61% Mismatches: 43  
Query Match: 56.10% Indels: 336  
DB: 2 Gaps: 5

US-10-047-021-86\_COPY\_28\_303 (1-276) x AC138284 (1-214559)

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Qy 107 -----ValLeuArgGluAaspPhe 112
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Qy 158 ----- 158
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Qy 159 -----ThrValSerGlySerLeuLeuMetAl 168
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DEFINITION ***
ACCESSION AC120636
VERSION AC120636.4 GI:25138029
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 223269)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
```



Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Dengon, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kwis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulsegged, H., Lozano, R.J., Lui, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwakoelameh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.O., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

## TITLE

Direct Submission

## JOURNAL

Unpublished

## AUTHORS

Worley, K.C.

## TITLE

Direct Submission

## JOURNAL

Submitted (09-MAY-2002)

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## REFERENCE

3

(bases 1 to 223269)

## AUTHORS

Rat Genome Sequencing Consortium.

## TITLE

Direct Submission

## JOURNAL

Submitted (20-NOV-2002)

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## COMMENT

On Nov 20, 2002 this sequence version replaced gi:23667909. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Aclas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature

## table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GXDD

Center clone name: CH230-136D4

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 201827 bases at least Q40

Consensus quality: 204782 bases at least Q30

Consensus quality: 206701 bases at least Q20

Estimated insert size: 209571; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 1 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submitter.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

\* 1 223269: contig of 223269 bp in length.

## FEATURES

## source

1. 223269

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/db\_xref="taxon:10116"

/clones="CH230-136D4"

478. 808

/note="clone boundary

clone\_end:Sp6

site:

end\_sequence:BH352255"

104879. 106665

/note="wgs contig"

164341. 165851

/note="wgs contig"

204100. 207640

/note="wgs contig"

221935. 223269

/note="wgs contig"

BASE COUNT 59410 a 47952 c 46732 g 54018 t 15157 others

## ORIGIN

US-10-047-021-86\_COPY\_28\_303 (1-276) x AC120636 (1-223269)

## Alignment Scores:

Pred. No.: 1.7e-36 Length: 223269

Score: 795.50 Matches: 204

Percent Similarity: 36.64% Conservativeness: 21

Best Local Similarity: 33.22% Mismatches: 46

Query Match: 53.93% Indels: 344

DB: 2 Gaps: 5

US-10-047-021-86\_COPY\_28\_303 (1-276) x AC120636 (1-223269)

Qy 2 AspSerProGlnIleLeuValHisProGlnAapGlnLeuPheGlnGlyPro 21

Db 202671 GATTCTCACCCAGATCTAGTATCATCCAGACAGCTACTTCAGGGCTCCGGGCG 202612

Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuAan 41

Db 202611 GCCAAGATGAGTTGCAGAGCATCGGGCCACCACCTTCCCATCGCTGCTGAAT 202552

Qy 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61

Db 202551 GGGCAGCCCTCAGCATGGCGACCCAGACCTACATTACCTCAATCAGATGGGACCTC 202492

Qy 62 LeuLeuLeuGlnProAlaArgGlyHisAlaHisSerGlyGln---AlaLeuSerThr 80  
Db 202491 CTGCTACATCGGCCCTTACCATGGAGCGCGGCAAGACGACGACATCTCTCAGCA 202432  
Qy 81 AspLeuGlyValThrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db 202431 ATCTGGGTGCTACACATGTGAGCCAGCAACCGGCTGGGCACAGCAGTGGCGGGT 202372  
Qy 101 AlaArgLeuSerValAla----- 106  
Db 202371 GCTAGGCTGTCTGTGGC-TGTGAGGCTTGGAGGGGTAGGCTCAGGGGTGAGGCAGAGTTA 202313  
Qy 106 ----- 106  
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Qy 106 ----- 106  
Db 202252 CGGTCTTGGGATGAAGTTAACTAGACATAAAGCGGCAAGGAAACCGGTACAGCAGAAC 202193  
Qy 106 ----- 106  
Db 202192 TGGGTAAGCGGTTAGGATAAGCAAGAGCTCGGGGTGGGTAGACATGCTTCCTGCTGAT 202133  
Qy 107 -----ValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
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Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProfiTrpGlyHisProGluPro 140  
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Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThr--- 159  
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Qy 159 ----- 159  
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Qy 176 \*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArg 195  
Db 201712 GGGACCTATATGTGTATGCCCAACCAATGCCGACACCGGAGAGTCCGGGCGCCAGG 201653  
Qy 196 ValSerIleGln----- 199  
Db 201652 GTGTCTATCCAGGGTAAGACAGGAGTGCATCTAAATCCAAATGAAGGCTCAGGAGATAAC 201593  
Qy 199 ----- 199  
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Qy 199 ----- 199  
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Db 201412 TGCTCACAAAAACAAGATGGAGAACAGCAGTAAGGGAGCTTTTGGCTTCCATAGCCAC 201353  
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Db 201352 GCTCACTCACATACACATGTGAACCCACACTCAAAGTGAAGCAAGTAGGAGACTC 201293  
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Qy 227 oAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\*TrpLys----- 242  
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Qy 242 ----- 242  
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Qy 243 -----ValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260  
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Qy 261 LeuProArgGluAlaArgGluLeuArgGlyGlnArg 272  
Db 200872 GGGACCCCGAGGACCGAGGATCTCCATGGACAGG 200837  
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LOCUS Rattus norvegicus clone CH230-85A24, WORKING DRAFT SEQUENCE.  
DEFINITION AC109983  
ACCESSION AC109983  
VERSION AC109983.5 GI-25006838  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 250318)  
AUTHORS Muzny, D., Marie, Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,  
Allen, C., Allen, H., Alsebrook, S., Amin, A., Angiano, D.,  
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
Bryant, N., Buha, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J.,  
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,  
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,  
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Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,  
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Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Louie, H., Lozano, R., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montanayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munitasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okunolu, G., Olampunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wiczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Direct Submission

Unpublished

2 (bases 1 to 250318)

Worley, K.C.

Direct Submission

Submitted (09-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 250318)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23266067. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GRFO

Center clone name: CH230-85A24

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 230810 bases at least Q40

Consensus quality: 233159 bases at least Q30

Consensus quality: 234781 bases at least Q20

Estimated insert size: 236162; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
\* This sequence will be replaced.  
\* By the finished sequence as soon as it is available and the accession number will be preserved.  
\* The accession number will be 250318 bp in length.

## FEATURES

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/clone="CH230-85A24"

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clone\_end:Sp6"

6097..7484

/note="wgs\_end\_extension"

clone\_end:Sp6"

10463..11371

/note="clone boundary"

clone\_end:Sp6"

site:

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/note="clone boundary"

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site:

end sequence: BH302237"

249161..250318

/note="wgs\_end\_extension"

clone\_end:T7"

BASE COUNT 66941 a 51524 c 51351 g 66227 t 14275 others

ORIGIN

Alignment Scores:

Pred. No.: 1.9e-36 Length: 250318

Score: 795.50 Matches: 204

Percent Similarity: 36.64% Conservative: 21

Best Local Similarity: 33.22% Mismatches: 46

Query Match: 53.93% Indels: 344

DB: 2 Gaps: 5

US-10-047-021-86\_COPY\_28\_303 (1-276) x AC109983 (1-250318)

Qy 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21

Db 129886 GATTCTCCACCCAGATCTTAGTTTCATCCCGAGCAGCTACTTTCAGGGCTCCGGGCG 129945

Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeuAen 41

Db 129946 GCCAAGATGAGTTCAGAGCATCGGGCCACCACTTCCCACTATCCGCTGCTGTAAT 130005

Qy 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61

Db 130006 GGGCAGCCCCCTCAGATGGCGACCCAGACCTTACCTACCTACATGAGTGGGACCTC 130065

Qy 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThr 80

Db 130066 CTGTACATCGGGCCCCCTTACCATGGAGCGGGCGGAGACGACCAACATTTCTCTCAGCA 130125

Qy 81 AspLeuGlyValThrThrCysGluAlaSerHisArgLeuGlyThrAlaValserArgGly 100

Db 130126 ATCTGGGTGTCTACATGTGAGCCAGCAACCGGCTGGGACAGCAGTGGCGGGGT 130185

Qy 101 AlaArgLeuSerValAla----- 106

Db 130186 GCTAGGCTGTCTGTGGC-TGGTGAGGCTTGGGAGGCTAGGCTAGGCTGAGGCTGAGGCTGAGTTA 130244

Qy 106 ----- 106

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Db 130245 GGCTGCGATGTTGTGTCACAGGAATACAGAGGCTCTATCTATGAAGGAGGCCCGGGTG 130304
Qy 106 ----- 106
Db 130305 CGGCTCTGGGATGAAGGTTAAACTAGACATAAACGGGCAAGAAACCGGTACAGCAGAAC 130364
Qy 106 ----- 106
Db 130365 TGGGTAAAGCGGTAGGATAAGCAAGACTCGGGTGGGTAGACATGCTTCTCGCTGAT 130424
Qy 107 ----- ValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
130425 CCGCTGACCTCCCAATAGTCTCCAGGAGACTTCGGATCCCAACCTCGGGACACAGTG 130484
Qy 121 AlaValValGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
130485 GCCGTGGTGGCGAGAGCTTGGTTCTCGAGTGTGCTCTCCCTGGGGCTACCCAAAGCCT 130544
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThr--- 159
130545 TCAGTCTCTGTGGAAGATGGGAACCCCTGGTCTCCAGCCAGGAGCGCACAGTG 130604
Qy 159 ----- 159
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Qy 159 ----- 159
Db 130665 AGCAACTGACCCGCTCTCCAGTGGCATGTCCCTTGGAAAGATCTGAGGACAGGAGGCAAG 130724
Qy 159 ----- 159
Db 130725 GAGACCTCAATATGCCCTCCGCCCTCTAAGTTTCTCACACTGAAGATTTCATGGAGTATT 130784
Qy 160 ----- ValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu 175
130785 TGACCTTGACAGGTGTCTGGGGATTCTCTGATGTGGCAAGCAGCAGAGAGAAATGACACG 130844
Qy 176 ***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArg 195
130845 GGGACCTATATGTGTATGGCCACCACAAATCCCGGACAAACGGGAGAGTCGGGCGCCAGG 130904
Qy 196 ValSerIleGln----- 199
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Qy 199 ----- 199
Db 130965 TCTGTGTGAACATGCTTGTCTTCATATATGTGAAGACTCAAGCAGCCAGCACCACATATA 131024
Qy 199 ----- 199
Db 131025 AAAGCAGACTATGACAGTGATGTGTGATTCAGTATCCAGTACAGACAAATGTGGAGTACAGAC 131084
Qy 199 ----- 199
Db 131085 AAGTGAATCCAGAAAGCTAGTAGACGGAAGAAGTCTGCCAGTGGGTTCCAGGTTTCAGTT 131144
Qy 199 ----- 199
Db 131145 TGTCTCACAAAAACAAGATGGAGNACAGCAGTAAGGGAGCTTTTGGCTTCCATAGCCAC 131204
Qy 199 ----- 199
Db 131205 GCTCACTCACATACACATGTGAACCCCACTCAAAGTGCAGGCAAAAGTAGGAGACTC 131264
Qy 199 ----- 199
Db 131265 CAGTTAGTGTGGTGGCCAGGATATGGGGTTTCAAGGTTCTCCCTATGTGAGGCTAGAACGCA 131324
Qy 199 ----- 199

Db 131325 CATAGGAATACTCTAGACCTGGAAACTCTGGAGCCAAAGTTTATCCAAGATGAAGATAGG 131384
Qy 200 ----- GluProGlnAspTyrThrGluPr 207
131385 TTCCACTCCTCCATCCCATCCCTGTGTGATCTCCCCACAGAGTCCACCGACCCACAAGGAGCA 131444
Qy 207 oValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspPr 227
131445 TCTAGAGCTTCTGGCTGTTTCAATTCAGCTGGAATAATGTGACCTGTCTGAACCCAGAACC 131504
Qy 227 oAlaGluGlyProLysProArgProAlaValTrpLeu***TrpLys----- 242
131505 TGTAAAGGCCCCCAAGCCTGGGCCAGCTGTGTGCTCAGCTGGAAGGTGAGGCAGAGGAC 131564
Qy 242 ----- 242
Db 131565 CCTGAAGACACGGAGAGCTCCCATGGACTCCCTAGTTCCCTGTCTTACTCTGACCTCTC 131624
Qy 243 ----- ValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
131625 CCCAGGTGAGGGGCCCTGTCTGCACCTGCGCCAGTCCAGTCATACACAGCCCTGTTCAGGGGCGCAGA 131684
Qy 261 LeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
131685 GGGACCCCGAGGAGCAGGGATCTCCATGGACAGAGG 131720
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Search completed: January 31, 2004, 14:37:34

Job time : 3137.42 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2004, 11:37:09 ; Search time 220.228 Seconds  
(without alignments)  
3383.062 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303  
Perfect score: 1475  
Sequence: 1 QDSPPQLVHPDQLFQPG.....SGPRLPREARELRGRRNTG 276

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO spool\_P/US10047021/runat\_30012004.145452.24552/app\_query.fasta\_1.910  
-DB=1\_Geneseq\_19Jun03 -QWTF=fascap -SUFFIX=rng -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=Blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLFMT=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10047021 @CGN 1.1 605 @runat\_30012004.145452.24552 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT\_DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_19Jun03:\*  
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24: /SIDS1/cgdata/geneseq/geneseq-emb1/NA2002.DAT:\*  
25: /SIDS1/cgdata/geneseq/geneseq-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result - No.	Score	Query Match	Length	DB	ID	Description
1	1469	99.6	1346	20	AAK51721	DNA encoding a hum
2	1469	99.6	1346	24	ABQ92573	Human secreted pro
3	1432	97.1	3267	24	ABN59723	Novel human coding
4	1432	97.1	3715	24	ABK87137	cDNA human ECSM4 p
5	1432	97.1	3716	20	AAZ34069	Human PRO860 nucle
6	1432	97.1	3716	21	AAZ78502	Human PRO860 (UNQ4
7	1432	97.1	3716	25	ABX92441	cDNA encoding huma
8	1432	97.1	3808	22	AAK51695	Human TANGO 330 fo
9	1424	96.5	4262	22	AAH18180	Human cDNA sequenc
10	1424	96.5	4262	22	AAH78073	Nucleotide sequenc
11	1077	73.0	3042	22	AAK01694	Human TANGO 330 fo
12	1062.5	72.0	3688	24	ABK87138	cDNA mouse ECSM4 p
13	1057	71.7	756	22	AAH08234	Human cDNA clone (
14	446.5	30.3	4291	20	AAV69278	Human T85 cDNA. H
15	446.5	30.3	4956	20	AAK55770	Human Robo 1 polyp
16	446.5	30.3	4956	20	AAK57253	Human ROBO1 cDNA.
17	404.5	27.4	6215	24	AAK49658	Human neurotransmi
18	396.5	26.9	6445	24	AAK49652	Human neurotransmi
19	395.5	26.8	4188	20	AAK55767	Drosophila Robo 1
20	395.5	26.8	4188	20	AAK57250	Drosophila ep. ROB
21	395.5	26.8	4355	23	ABL22881	Drosophila melanog
22	354.5	24.0	3894	20	AAK55769	C. elegans Robo po
23	354.5	24.0	3894	20	AAK57252	C. elegans Robo cd
24	347	23.5	2499	23	ABL09471	Drosophila melanog
25	345	23.4	4146	20	AAK55768	Drosophila Robo 2
26	345	23.4	4146	20	AAK57251	Drosophila ep. ROB
27	307	20.8	2658	23	ABL09371	Drosophila melanog
28	292.5	19.8	8410	23	ABL22880	Drosophila melanog
29	276.5	18.7	5510	21	AAZ51671	Human PS3 target m
30	276.5	18.7	5510	24	ABK83723	Human cDNA differe
31	276.5	18.7	5510	24	ABN95260	Gene #1758 used to
32	276.5	18.7	5510	25	ABX08782	Angiogenesis-assoc
33	276.5	18.7	5530	22	ABA08831	Human peroxidasin
34	276.5	18.7	6814	24	ABV70409	Human bone remodel
35	276.5	18.7	6847	20	ABV99922	Melanoma associate
36	276.5	18.7	6847	24	ABQ88160	Human osteoblast d
37	275.5	18.7	4694	22	AAK51847	Human polynucleoti
38	267.5	18.1	4080	25	AAK49595	Human cytoskeleton
39	267.5	18.1	4131	25	ABT16046	NOVX related polyn
40	267.5	18.1	4360	25	AAK49596	Human cytoskeleton
41	267.5	18.1	4739	22	AAK51848	Human polynucleoti
42	265.5	18.0	5093	24	AAK39621	Human secreted pro
43	259	17.6	5164	23	ABL01909	Drosophila melanog
44	256	17.4	4548	24	AAI64283	Human transient ax
45	256	17.4	11796	25	ABX10231	Human cDNA encodin

ALIGNMENTS

RESULT 1  
AAK51721  
ID AAK51721 standard; DNA; 1346 BP.  
XX  
AC AAK51721;  
XX  
DT 17-JUN-1999 (first entry)  
XX  
DE DNA encoding a human secreted protein.  
XX  
KW Human secreted protein; cancer; immune disorder; infection;  
KW inflammatory disorder; skin disorder; tumour; atherosclerosis;  
KW reestenosis; autoimmune disorder; Alzheimer's disease;  
KW peripheral neuropathy; trauma; spinal cord injury; allergy;  
KW hematopoietic disorder; skeletal disorder; neurological disorder;  
KW arthritic disorder; asthma; immunodeficiency disease; AIDS;  
KW transplant rejection; ss.

```
XX OS Homo sapiens.
XX WO9911293-A1.
XX PD 11-MAR-1999.
XX PF 03-SEP-1998; 98WO-US18360.
XX PR 12-SEP-1997; 97US-0058974.
XX PR 05-SEP-1997; 97US-0057626.
XX PR 05-SEP-1997; 97US-0057663.
XX PR 12-SEP-1997; 97US-0058666.
XX PR 12-SEP-1997; 97US-0058667.
XX PR 12-SEP-1997; 97US-0058667.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;
XX PI Rosen GA, Ruben SM, Shi Y;
XX DR WPI; 1999-204988/17.
XX DR P-PSDB; AAY12934.
XX PT New isolated human genes and the secreted polypeptides they encode
XX PT - useful for diagnosis and treatment of e.g. neurological disorders,
XX PT tumours, immune disorders, inflammation or haematological disorders
XX PS Claim 1; Page 165-166; 215pp; English.
XX CC AAX51701-55 encode human secreted proteins. The polynucleotides and
XX CC their corresponding secreted polypeptides are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g. by protein or gene
XX CC therapy. Pathological conditions can also be diagnosed by determining the
XX CC the amount of the new polypeptides in a sample or by determining the
XX CC presence of mutations in the new polynucleotides. Specific uses are
XX CC described for each polynucleotide, based on which tissues they are
XX CC most highly expressed in, and include developing products for the
XX CC diagnosis or treatment of cancer, immune disorders, infection,
XX CC inflammatory disorders, skin disorders, tumours, atherosclerosis,
XX CC restenosis, autoimmune disorders, Alzheimer's disease, peripheral
XX CC neuropathies, trauma, spinal cord injuries, allergy, hematopoietic
XX CC disorders, skeletal disorders neurological disorders, arthritic
XX CC disorders, asthma, immunodeficiency diseases, AIDS and transplant
XX CC rejection. The polypeptides are also useful for identifying their
XX CC binding partners.
XX SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 6 other;

Alignment Scores:
Pred. No.: 9.12e-91 Length: 1346
Score: 1469.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.55% Indels: 0
DB: 20 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AAX51721 (1-1346)
QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
DB 112 CAGGACTCCCGCCCCAGATCTTAGTCCACCCCGAGGACGAGTGTCCAGGGCCCTGGC 171
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
DB 172 CTGCGCAGGATGAGTCCGAGCCTCAGCCAGCCACCTCCACCATCCGCTGGTGGTG 231
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
DB 232 AATGGGAGCCCCCTGAGCATGTGGTCCCCCAGACCCACACACCTCTGCTGATGGGACC 291
QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
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DB 292 CTTCTGCTGTACAGCCCCCTGCGGGGACATGCCACCATGCGCAGGCGCTGTCCACA 351
QY 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
DB 352 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCAGTCCAGCAGGC 411
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
DB 412 GCTCGGCTGTCTGTGGCTGTCTCCGGGAGATTTCCAGATCCAGCTCCGGACATGGTG 471
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProProTrpGlyHisProGluPro 140
DB 472 GCTGTGGTGGTGGAGCAGTCTTACTCTGGAATGTGGGCGCCCTGGGGCCACCCAGAGCCC 531
QY 141 ThrValSerTrpTrpIysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 532 ACAGTCTCATGTGGTGGAAAGATGGAAACCCCTCGCCCTCCAGCCCGGAAGGCACACAGTG 591
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
DB 592 TCCGGGGGTCTCTGTGTGATGGCAAGACGACAGAGTGCAGNANGGACCTACATGTGT 651
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
DB 652 GTGCCACCAACAGCGCAGCACACAGGAGAGCGCGCGCAGCGCGGTTCCTATCCAGGAG 711
QY 201 ProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
DB 712 CCCGAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGGAAATTCAGCTGGAAAAATGTG 771
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
DB 772 ACTCTCTGAACCCGGATCTCTGAGARGGCCCCAGCCTAGACCGCGGTGTGCTCARG 831
QY 241 TrpIysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
DB 832 TGGAAAGTCTAGTGGCCCTTGGCCCTGCCCAATCTTACACGGCTTGTTCAGGACCCAGA 891
QY 261 LeuProArgGluAlaArgGluLeuArgGlyGlnArgArgAsnThrGly 276
DB 892 CTGCCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGGAGGAACACACAGGA 939

RESULT 2
ABQ92573
ID ABQ92573 standard; cDNA; 1346 BP.
XX AC ABQ92573;
XX DT 12-NOV-2002 (first entry)
XX DE Human secreted protein encoding cDNA SEQ ID NO 31.
XX KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
XX KW gene; ss.
XX OS Homo sapiens.
XX PN WO200257420-A2.
XX PD 25-JUL-2002.
XX PF 17-JAN-2002; 2002WO-US01109.
XX PR 18-JAN-2001; 2001US-262066P.
XX PR (HUMA-) HUMAN GENOME SCI INC.
```

XX Moore PA, Ruben SM, LaFleur DW, Shi Y, Rosen CA, Olsen H;  
PI Ebner R, Brewer LA;  
XX WPI: 2002-599716/64.  
DR P-PSDB; ABP62033.  
XX  
XX New polynucleotides and polypeptides useful for diagnosing, prognosing,  
PT treating or preventing e.g. neurodegenerative, central nervous system,  
PT autoimmune, respiratory, reproductive, or inflammatory diseases or  
PT disorders  
XX  
PS Claim 1; Page 713-714; 785pp; English.  
XX  
XX The invention relates to novel genes (ABQ92553-ABQ92607) and proteins  
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful  
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections.  
XX  
SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 6 other;

Alignment Scores:  
Pred. No.: 9,128-91 Length: 1346  
Score: 1469.00 Matches: 276  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.59% Indels: 0  
DB: 24 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x ABQ92573 (1-1346)

Qy 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db 112 CAGGACTCCCGCCCGACATCTTAGTCCACCCAGGACCAGCTGTTCCAGGGCCCTGGC 171  
Qy 21 ProAlaArgMetSerCyArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40  
Db 172 CTTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCTCCACCATCCGCTGTGCTG 231  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db 232 AATGGCAGCCCTGAGCATGTGTCGCCAGACCACACACCTCTCTGCTGATGGGACC 291  
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db 292 CTCTCTGCTACAGCCCTGCCCGGGGACATGCCACGATGGCCAGGCCCTGTCCACA 351  
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db 352 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGCTTGGCAGCCAGTCAGCAGAGGC 411  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db 412 GCTCGGCTGTCTGTGGCTGTCTCGGGAGGATTTCCAGATCCAGCCCTCGGGACATGTG 471  
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140  
Db 472 GCTGTGTGGGTGACAGATTACTCTGGATGTGGGGCCCTCGGGGCCACCCAGAGGCC 531  
Qy 141 ThrValSerTrpTrpLysAspGlyProLeuAlaLeuGlnProGlyArgHisThrVal 160  
Db 532 ACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTGTG 591

Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCys 180  
Db 592 TCCGGGGGTCCCTGCTGATGTGCAAGAGCAGAGAGAGTGAACGAAGGACCTACATGTGT 651  
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
Db 652 GTGCCCAACCAACAGCGCAGGACACAGGAGAGCGCGCAGCCCGGTTTCCATCCAGAG 711  
Qy 201 ProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220  
Db 712 CCCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 771  
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\* 240  
Db 772 ACACCTCTGAACCCGGATCCTGTGAGAGCGGCCCAAGCCTAGACCGGGGTGTGGCTCARG 831  
Qy 241 TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260  
Db 832 TGGAAAGTCAAGTGGCCCTTGTGCGCTGCCCAATCTTACACGGCCTTGTTCAGGACCC 891  
Qy 261 LeuProArgGluAlaArgGluLeuArgGlyGlnArgArgAsnThrGly 276  
Db 892 CTGCCCCGGAGCGCAGGAGCTCCGTGGCGAGAGGAGGAAACACAGGA 939  
RESULT 3  
ID ABN59723 standard; cDNA; 3267 BP.  
XX AC ABN59723;  
XX 28-JUN-2002 (first entry)  
XX Novel human coding sequence SEQ ID NO: 134.  
XX Human; antianaemic; vulnery; antiinflammatory; immunomodulator;  
KW antinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
KW neuroprotective; antiparkinsonian; protein therapy; EST;  
KW expressed sequence tag; gene; ss.  
XX Homo sapiens.  
XX WO200222660-A2.  
XX 21-MAR-2002.  
XX 10-SEP-2001; 2001WO-US26015.  
XX 11-SEP-2000; 2000US-0659671.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren P;  
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
XX WPI: 2002-292408/33.  
XX P-PSDB; ABB97310.  
XX An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis -  
XX  
XX Claim 1; SEQ ID NO 134; 509pp; English.  
XX The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibit e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat  
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions  
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC parkinson's disease. The present sequence is a coding sequence of the



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CC invention.
XX
SQ Sequence 3267 BP; 628 A; 1101 C; 927 G; 611 T; 0 other;

Alignment Scores:
Pred. NO.: 7.36e-88 Length: 3267
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 24 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x ABN59723 (1-3267)

Qy 1 GlnAspSerProGlnIleuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db |||||
Qy 116 CAGGACTCCCGCCCGCCAGATCTAGTCACCCCGAGGACGCTGTTCCAGGGCCCTGGC 175
Db |||||
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db |||||
Qy 176 CTGCGCAGGATGAGTGCAGAGCCTCAGGCCAGCCACTCCACCATCCGCTGCTGTG 235
Db |||||
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db |||||
Qy 236 AATGGGAGCCCTCAGCATGTGTCGCCCGGAGCATGCCACGATGGCCAGCCCTCTGATGGGACC 295
Db |||||
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db |||||
Qy 296 CTTCTGCTGTACAGCCCGCCCGGAGCATGCCACGATGGCCAGCCCTCTGTCACA 355
Db |||||
Qy 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db |||||
Qy 356 GACCTGGGTGCTACATGTGAGCCGACGCAACCGCTTGCACGGCAGTCAGCAGGCG 415
Db |||||
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db |||||
Qy 416 CTTGGTGTCTGTGGTGTCTCTCGGAGGATTTCCAGATCCAGCCTCGGAGCATGGTG 475
Db |||||
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGlyPro 140
Db |||||
Qy 476 GCTGTGGTGGTGAGCAGTTTACTGTGAATGTGGCGCCCTGGGGCCACCCAGAGCCC 535
Db |||||
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db |||||
Qy 536 ACAGTCTCATGTGGAAAGATGGGAACCCCTGGCCCTCCAGCCCGGAGGCACACAGTG 595
Db |||||
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyMetCys 180
Db |||||
Qy 596 TCCGGGGGTCCTGTCTGATGGCAAGAGCAGAGAAGAGTGCAGGAAGGACCTACATGTGT 655
Db |||||
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db |||||
Qy 656 GTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCCGGGTTTCATCCAGGAG 715
Db |||||
Qy 201 ProGlnAspTyThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db |||||
Qy 716 CCCAGGACTACAGGAGCCTGTGGAGCTTCTGCTGTGCGAATTCAGCTGGAAATGTG 775
Db |||||
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db |||||
Qy 776 ACACCTGTGAACCGGATCTCTGACAGAGGGGCCCAAGCCTAGACCGGGCGGTGTGCTCAGC 835
Db |||||
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
Db |||||
Qy 836 TGGAGAGTGTAGTGGCCCTGTGCGCTCTGCCAAATCTTACAGGGCTTGTTCAGGACCCAG 895
Db |||||
Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db |||||
Qy 896 ACTGCCCGGAGGCCAGGAGCTCCGTGGGCAGAGG 932
Db |||||

RESULT 4
ABK87137
ID ABK87137 standard; cDNA; 3715 BP.
```

```
XX
AC ABK87137;
XX
DT 07-OCT-2002 (first entry)
XX
DE cDNA human ECSM4 protein.
XX
KW Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW imaging vascular endothelium; proliferative disease; cancer;
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
KW endothelial damage; tumour neovasculature; cardiac disease;
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
KW cardiant; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 70..3384
FT /*tag= a
FT /product= "ECSM4"
XX
XX W020236771-A2.
XX
PD 10-MAY-2002.
XX
XX 06-NOV-2001; 2001WO-GB04906.
XX
XX 06-NOV-2000; 2000US-245566P.
XX 07-MAR-2001; 2001US-273662P.
XX
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
XX Bicknell R, Huminiecki L;
XX
XX WPI; 2002-508120/54.
XX P-PSDB; AAU99419.
XX
XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
XX imaging, diagnosing and treating a condition involving vascular
XX endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
XX
XX Disclosure; Fig 12; 248pp; English.
XX
XX The present invention relates to endothelial cell-specific molecule 4
XX (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
XX proteins are useful for imaging vascular endothelium in the body of
XX an individual, and for diagnosing and treating a proliferative
XX disease or condition involving the vascular endothelium (preferably,
XX neovasculature) such as cancer, psoriasis, diabetic retinopathy,
XX atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in
XX the manufacture of diagnostic or prognostic agent for such conditions.
XX The proteins are also useful for detecting endothelial damage or
XX activation, detecting a tumour or tumour neovasculature, cardiac
XX disease, or endometriosis by detecting the amount of ECSM4 present in
XX a sample. The polynucleotide sequences encoding ECSM4 are useful in
XX gene therapy for treating a hypoxic condition such as cancer, cardiac
XX disease, endometriosis or atherosclerosis and in the manufacture of
XX medicaments for treating the above disease. The sequences are useful
XX for modulating angiogenesis in an individual. The present sequence
XX encodes human ECSM4 protein.
XX
XX Sequence 3715 BP; 725 A; 1239 C; 1053 G; 698 T; 0 other;

Alignment Scores:
Pred. No.: 8.42e-88 Length: 3715
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 24 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x ABK87137 (1-3715)
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Qy 1 GlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db 151 CAGGACTCCCGCCCGCAGATCTAGTCCACCCCGAGGACAGCTGTTCAGGGCCCTGGC 210  
Qy 21 ProAlaAatqMetSerCyeArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40  
Db 211 CTGCGCAGGATGAGTGCACAGCCTCAGGCGCAGCAGCCTCCACCATCGCTGGTGTGTG 270  
Qy 41 AenGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db 271 NATGGGAGCCCTGAGCATGTGTGCCCCAGACCCACACCATCTCTGCTGATGGGACC 330  
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db 331 CTTCTGCTCTACAGCCCTCCCGGGGACATGCCCCAGATGGCCAGCCCTGTCCACA 390  
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db 391 GACCTGGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCATGACGAGGC 450  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db 451 GCTGGGCTGTGTGGTGTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGCACATGGTG 510  
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140  
Db 511 GCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGGCCCGCCCTGGGGCCACCCAGAGGCC 570  
Qy 141 ThrValSerTrpTrpIleAspGlyCysProLeuAlaLeuGlnProGlyArgHisThrVal 160  
Db 571 ACAGTCTCATGTGTGAAAGATGGGAAACCCCTGGGCCCTCCAGCCCGGAAGGCACACAGTG 630  
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCys 180  
Db 631 TCCGGGGGCTCCTGCTGTATGTCACAGACAGAGAGTGCAGAGGACCTACATGTGT 690  
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
Db 691 GTGGCCACCAACAGCGCAGCATAGGAGAGCGCGCAGCCGGTTCATCCAGGAG 750  
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220  
Db 751 CCCCAGGACTACACGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 810  
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\* 240  
Db 811 ACACCTGCTGAACCCGGATCTCGAGAGGCCCCAAGCCTAGACCGCGGTGTGGCTCAGC 870  
Qy 241 TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260  
Db 871 TGGAGGTCAGTGGGCCCTGCTGGCTGCCCCAATCTTACACGGCTTGTTCAGGACCCAG 930  
Qy 260 GlnProArgGluAlaArgGluLeuArgGlyGlnArg 272  
Db 931 ACTGCCCCGGGAGCGGAGGAGCTCGTGGGCAGAGG 967  
RESULT 5  
AAZ34069  
ID AAZ34069 standard; cDNA; 3716 BP.  
XX AC AAZ34069;  
XX DT 07-DEC-1999 (first entry)  
XX DE Human PRO860 nucleotide sequence.  
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.  
XX OS Homo sapiens.  
XX PN WO9946281-A2.

XX 16-SEP-1999.  
PD 08-MAR-1999; 99WO-US05028.  
XX 10-MAR-1998; 98US-0077450.  
PR 11-MAR-1998; 98US-0077632.  
PR 11-MAR-1998; 98US-0077641.  
PR 11-MAR-1998; 98US-0077649.  
PR 12-MAR-1998; 98US-0077791.  
PR 13-MAR-1998; 98US-0078004.  
PR 17-MAR-1998; 98US-0040220.  
PR 20-MAR-1998; 98US-0078886.  
PR 20-MAR-1998; 98US-0078910.  
PR 20-MAR-1998; 98US-0078936.  
PR 20-MAR-1998; 98US-0078939.  
PR 25-MAR-1998; 98US-0078939.  
PR 26-MAR-1998; 98US-0079294.  
PR 26-MAR-1998; 98US-0079656.  
PR 27-MAR-1998; 98US-0079663.  
PR 27-MAR-1998; 98US-0079664.  
PR 27-MAR-1998; 98US-0079689.  
PR 27-MAR-1998; 98US-0079728.  
PR 27-MAR-1998; 98US-0079786.  
PR 30-MAR-1998; 98US-0079920.  
PR 30-MAR-1998; 98US-0079923.  
PR 31-MAR-1998; 98US-0080105.  
PR 31-MAR-1998; 98US-0080107.  
PR 31-MAR-1998; 98US-0080165.  
PR 31-MAR-1998; 98US-0080194.  
PR 01-APR-1998; 98US-0080327.  
PR 01-APR-1998; 98US-0080328.  
PR 01-APR-1998; 98US-0080333.  
PR 01-APR-1998; 98US-0080334.  
PR 08-APR-1998; 98US-0081049.  
PR 08-APR-1998; 98US-0081070.  
PR 08-APR-1998; 98US-0081071.  
PR 09-APR-1998; 98US-0081195.  
PR 09-APR-1998; 98US-0081203.  
PR 09-APR-1998; 98US-0081229.  
PR 15-APR-1998; 98US-0081817.  
PR 15-APR-1998; 98US-0081838.  
PR 15-APR-1998; 98US-0081952.  
PR 15-APR-1998; 98US-0081955.  
PR 21-APR-1998; 98US-0082568.  
PR 21-APR-1998; 98US-0082569.  
PR 22-APR-1998; 98US-0082700.  
PR 22-APR-1998; 98US-0082704.  
PR 22-APR-1998; 98US-0082804.  
PR 23-APR-1998; 98US-0082767.  
PR 23-APR-1998; 98US-0082796.  
PR 27-APR-1998; 98US-0083336.  
PR 28-APR-1998; 98US-0083322.  
PR 29-APR-1998; 98US-0083392.  
PR 29-APR-1998; 98US-0083495.  
PR 29-APR-1998; 98US-0083496.  
PR 29-APR-1998; 98US-0083499.  
PR 29-APR-1998; 98US-0083500.  
PR 29-APR-1998; 98US-0083545.  
PR 29-APR-1998; 98US-0083554.  
PR 29-APR-1998; 98US-0083558.  
PR 29-APR-1998; 98US-0083559.  
PR 30-APR-1998; 98US-0083742.  
PR 05-MAY-1998; 98US-0084366.  
PR 06-MAY-1998; 98US-0084414.  
PR 06-MAY-1998; 98US-0084441.  
PR 07-MAY-1998; 98US-0084598.  
PR 07-MAY-1998; 98US-0084600.  
PR 07-MAY-1998; 98US-0084627.  
PR 07-MAY-1998; 98US-0084637.  
PR 07-MAY-1998; 98US-0084639.  
PR 07-MAY-1998; 98US-0084640.  
PR 07-MAY-1998; 98US-0084643.  
PR 13-MAY-1998; 98US-0085323.

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PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX (GETH ) GENENTECH INC.
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX P-PSDB; AAY41716.
XX WPI; 1999-551358/46.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Claim 2; Fig 76; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AAZ33891 to
XX AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX
XX SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;

Alignment Scores:
Pred. No.: 8.42e-88 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 20 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x AAZ34069 (1-3716)

Qy 1 GlnAepSerProGlnIleLeuValHisProGlnAepGlnLeuPheGlnGlyProGly 20
Db 73 CAGGACTCCCGCCCGCAGATCTAGTCCACCCCGCAGGACCACTGTTCCAGGGCCCTGGC 132
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 133 CCTGCCAGGATGAGTGCACAGCCCTCAGCCAGCCACCTCCACCATCCGCTGGTGTG 192
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGCAGCCCTCGAGCATGCTGCCCGCCAGCCACCACTCCCTCGCTGATGGGACC 252
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 253 CTTCTGCTGTACAGCCCGCCCTGCGCGGGGACATGCCACGATGCCAGGCCCTGTCCACA 312
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Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTCTTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGC 372
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 373 GCTCGGCTGTCTGGGTGCTCTCCGGGAGGATTTCCAGATCCAGACCTCGGGACATGTTG 432
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 433 GCTGTGGTGGGTGAGCAGTCTTACTCTGGAATGTGGCGCCGCTGGGGCCACCCAGAGCCC 492
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 493 ACAGTCTCATGTGGGAAGATGGGAACCCCTGGCCCTCCAGCCCGGAGGACACACAGTG 552
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGlyLysSerAspGlu***ThrTyrMetCys 180
Db 553 TCCGGGGGGTCCCTGCTGATGGCAAGAGACAGAGAGAGTGCAGGAAGGACCTACATGTGT 612
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 613 GTGGCCACCAACAGCGCAGGACATAGGGAGAGCGCGCGCGGTTTCATCCAGAG 672
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 673 CCCAGGACTACACGGAGCCCTGTGGAGTCTTGGCTGTGCAATTCAGCTGGAAAATCTG 732
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 733 ACCTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGGGCGGTGGCTCAGC 792
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 793 TGAAGGTCAGTGGCCCTGTGGCGCTGCCCAATCTTACAGCGCTTGTTCAGGACCCAG 852
Qy 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 853 ACTGCCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 889
XX
XX RESULT 6
XX AAC78502
XX ID AAC78502 standard; cDNA; 3716 BP.
XX AC AAC78502;
XX XX
XX DT 08-FEB-2001 (first entry)
XX DE Human PRO860 (UNQ421) nucleotide sequence SEQ ID NO:210.
XX KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
XX KW expressed sequence tag; detection; cancer; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200053756-A2.
XX PD
XX PF 14-SEP-2000.
XX PP 18-FEB-2000; 2000WO-US04341.
XX XX
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 12-MAR-1999; 99US-0123957.
XX PR 29-MAR-1999; 99US-0126773.
XX PR 21-APR-1999; 99US-0130232.
XX PR 28-APR-1999; 99US-0131445.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 29-OCT-1999; 99US-0162506.
XX PR 30-NOV-1999; 99WO-US28313.
XX PR 02-DEC-1999; 99WO-US28551.
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PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA;  
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
XX  
XX  
DR WPI: 2000-611443/58.  
DR P-PSDB; AAB44272.  
XX  
XX  
PT Novel PRO polypeptides and polynucleotides used in detection methods,  
PT to target bioactive molecules to specific cells, and to modulate  
PT cellular activities -  
XX  
XX  
PS Claim 2; Fig 76; 636pp; English.  
XX  
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
CC sequence tag) sequences which encode secreted or transmembrane PRO  
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
CC activity. The polynucleotides and polypeptides can be used for detecting  
CC the presence of PRO polypeptides in samples, for linking bioactive  
CC molecules to cells and for modulating biological activities of cells,  
CC using the polypeptides for specific targeting. The polypeptide targeting  
CC can be used to kill the target cells, e.g. for the treatment of cancers.  
CC The polypeptide pairs provide specific targeting of bioactive molecules  
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
CC the isolation of the PRO polynucleotide sequences.  
XX  
SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;

Alignment Scores:  
Pred. No.: 8,42e-88 Length: 3716  
Score: 1432.00 Matches: 268  
Percent Similarity: 98.53% Conservative: 1  
Best Local Similarity: 98.17% Mismatches: 3  
Query Match: 97.08% Indels: 1  
DB: 21 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x AAC78502 (1-3716)

QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
DB 73 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGCCAGGACGAGCTTTCAGGGCCCTGGC 132  
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40  
DB 133 CCGCCAGGATGAGTGCACAGCCTCAGGCGAGCCACCTCCACCATCCGCTGGTGTG 192  
QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
DB 193 AATGGGAGCCCTGAGCATGTGTGCGCCAGACCCACACACCATCTCTGCTGATGGAGCC 252  
QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
DB 253 CTTCTGCTGTACAGCCCTGCGCCGGGACATGTCACGATGGCCAGGCTGTTCACA 312  
QY 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgly 100  
DB 313 GACCTGGGTGTACACATGTGAGGCCAGCAACCGGCTGGCAGCGAGTCAGCAGAGGC 372  
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
DB 373 GCTCGGCTGTCTGTGGCTGTCTCTCCGGGAGGATTTCCAGATCCAGCCTCGGACATGTTG 432

QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140  
DB 433 GCTGTGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGGCCACCCAGAGCCC 492  
QY 141 ThrValSerTrpTrpTyrAspGlyValProLeuAlaLeuGlnProGlyArgHisThrVal 160  
DB 493 ACAGTCTCATGTGTGGAAGATGGGAAACCCCTGGCCCTTCCAGCCCGGAAGCACACAGTG 552  
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCys 180  
DB 553 TCCGGGGGGTCCCTGCTGTGTGTCAGAGCAGAGAGAGTGCAGAGGACCTACATGTGT 612  
QY 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaAaGValSerIleGlnGlu 200  
DB 613 GTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCGCGGTTTCCATCCAGGAG 672  
QY 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220  
DB 673 CCCGAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTG 732  
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\* 240  
DB 733 ACATCTGTGAACCCGGATCTCTGCAGAGGGCCCCAAGCCTAGACCGCGGTGTGGCTCAGC 792  
QY 241 TrpLysValSerGlyPro\*\*\*-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260  
DB 793 TGGAAAGGTCACTGGCCCTGTGCTGCGCTGCCCAATCTTACACGCGCTTGTTCAGGACCCAG 852  
QY 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272  
DB 853 ACTCGCCCGGAGGCCAGGAGCTCCGTGGGCAGAGG 889

RESULT 7  
ABX92441  
ID ABX92441 standard; cDNA; 3716 BP.  
AC ABX92441;  
XX  
XX  
DT 08-MAY-2003 (first entry)  
XX  
DE cDNA encoding human PRO860 polypeptide.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
KW cardiac insufficiency; nervous system disorder; kidney disorder;  
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;  
KW genetic disorder; cytostatic; antidiabetic; anti-inflammatory;  
KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;  
KW cardiant; gene; 88.  
XX  
OS Homo sapiens.  
XX  
XX US2002169284-A1.  
XX  
PD 14-NOV-2002.  
XX  
PF 16-OCT-2001; 2001US-0978697.  
XX  
PR 07-OCT-1998; 98WO-US21141.  
PR 20-NOV-1998; 98WO-US24855.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US31243.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.

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PR 06-JAN-2000; 200WO-US00376.
PR 11-FEB-2000; 200WO-US03565.
PR 18-FEB-2000; 200WO-US04341.
PR 24-FEB-2000; 200WO-US05004.
PR 02-MAR-2000; 200WO-US05841.
PR 10-MAR-2000; 200WO-US06319.
PR 21-MAR-2000; 200WO-US07532.
PR 30-MAR-2000; 200WO-US08439.
PR 17-MAY-2000; 200WO-US13705.
PR 22-MAY-2000; 200WO-US14042.
PR 30-MAY-2000; 200WO-US14941.
PR 02-JUN-2000; 200WO-US15264.
PR 28-JUL-2000; 200WO-US20710.
PR 24-AUG-2000; 200WO-US23328.
PR 01-DEC-2000; 200WO-US32678.
PR 20-DEC-2000; 200WO-US34956.
PR 28-FEB-2001; 200WO-US06520.
PR 22-MAR-2001; 200WO-US09552.
PR 25-MAY-2001; 200WO-US17092.
PR 01-JUN-2001; 200WO-US17800.
PR 20-JUN-2001; 200WO-US19692.
PR 29-JUN-2001; 200WO-US21066.
PR 09-JUL-2001; 200WO-US21735.
PR 17-OCT-1997; 97US-062250B.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-004022D.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.

XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR P-PSDB; ABUG1102.
XX
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating cancer, kidney diseases, bone,
XX cartilage disorders and immune deficiencies -
XX
XX Claim 2; Fig 76; 459pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The
XX PRO polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for
XX linking bioactive molecules to cells expressing PRO polypeptides,
XX for modulating biological activities of cells expressing PRO
XX polypeptides, and for identifying agonists or antagonists. The
XX bioactive molecule may be a toxin, radiolabel or antibody, and causes
XX apoptosis or death of the cell. The PRO polypeptides are useful for
XX treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
XX cardiac insufficiency, nervous system disorders, kidney disorders,
XX bone and cartilage disorders or arthritis, tumours, and wound healing.
XX The polynucleotide sequences encoding PRO polypeptides are useful as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, in the preparation of PRO polypeptides, for
XX generating transgenic animals or knockout animals, and for the genetic
XX analysis of individuals with genetic disorders, and in gene therapy.
XX Note: The sequence data for this patent was obtained in electronic
XX format directly from the USPTO web site at
XX seqdata.uspto.gov/psipsDIDENTry.html.
SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;

Alignment Scores:
Pred. No.: 8.42e-88 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservatives: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 25 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x ABX92441 (1-3716)
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Db 73 CAGGACTCCCGCCGCCAGATCCTAGTCCACCCCGAGCCAGCTGTTCACGGGCGCTGGC 132
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 133 CCTGCCAGGATGAGCTGCCAAGCCCTCAGGCCAGCCACCTCCCATCCGCTGGTGTCTG 192
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGGCGAGCCCTGAGCATGGTGTCCCGCCAGAGCCACACACCTCTCCGTATGGGACC 252
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 253 CTTCTGTGTACAGCCCTCTGCCCGGGGAGCATGCCACCATGGCCAGGCGCTGTCCACA 312
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTGTCTACATGTGAGGCCAGCAACCGGTGTGCACGGCAGTCAGCAGAGGC 372
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnInLeuProArgAspMetVal 120
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Db 373 GCTCGGCTCTGTGGCTCTCTCGGGAGGATTTCCAGATCCAGCTCGGACATGGTG 432
Qy 121 AlaValValGluGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140
Db 433 GCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGGCCCTCGGGCCACCAGAGCCC 492
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 493 ACAGTCTCATGTGTGGAAGATGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTG 552
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
Db 553 TCCGGGGGTCCCTGCTGATGCAAGACAGACAGAGAGTGACGAAGGACCTACATGTGT 612
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 613 GTGGCCACCAACAGCCAGACAGACATAGGGAGAGCCGGCCAGCCGGTTTCCATCCAGGAG 672
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluVal 220
Db 673 CCCAGGACTACAGCGAGCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAATGTG 732
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 733 ACACGTCTGAACCGGATCTCGACAGAGGCCCAAGCCCTAGACCCGGCGTGTGGCTCAGC 792
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
Db 793 TGGAAAGGTCAAGTGGCCCTCTCGCGCTGCCCAATCTTACAGCGCCTTGTTCAGGACCCAG 852
Qy 260 GLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
Db 853 ACTGCCCGGGAGGCCAGCGAGCTCCGTGGGCAGAGG 889
RESULT 8
AAS01695
ID AAS01695 standard; cDNA; 3808 BP.
AC AAS01695;
XX
XX 18-JUL-2001 (first entry)
DE Human TANGO 330 form 2 cDNA sequence.
KW Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; astrocyte; cancer; ss;
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 9..1451
FT /tag= a
FT /product= "TANGO 330 form 2 protein"
FT /note= "The ORF is specifically claimed"
FT sig_peptide 9..68
FT /tag= b
FT mat_peptide 69..1448
FT /tag= c
XX
XX WO200123523-A2.
XX
XX 05-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US27202.
XX
XX 30-SEP-1999; 99US-0409634.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kirst S, Wrighton N, Fraser CC;
```

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XX WPI; 2001-235372/24.
DR P-PSDB; AAU00501.
XX
XX Isolated secreted proteins and their encoding nucleic acids are used
PT for diagnosis and treatment of e.g. bacterial and viral infections,
PT autoimmune diseases and inflammatory disorders -
XX
XX Claim 2; Fig 14; 261pp; English.
XX
XX The present sequence encoding for human TANGO 330 form 2 is
CC isolated from cDNA clone Jthx181e12 from a human astrocyte cDNA
CC library. TANGO 330 is 1 of 4 novel human transmembrane proteins
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
CC are useful as modulating agents in regulating a variety of cellular
CC processes and can be used to express the proteins in a host cell in
CC gene therapy applications. Antisense nucleic acid molecules and
CC expression vectors containing the TANGO nucleic acids are also described.
CC Diagnostic assays can be used to detect genetic alterations in the TANGO
CC nucleic acids and to identify compounds that bind to or modulate activity
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
CC monitor protein levels in tissue as a clinical testing procedure.
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
CC and proteins may be used to diagnose, treat and monitor disorders of the
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
CC can also be used to treat cell proliferative disorders (e.g. cancer),
CC and neurological disorders e.g. Alzheimer's disease.
XX
XX SQ Sequence 3808 BP; 773 A; 1244 C; 1041 G; 750 T; 0 other;
```

## Alignment Scores:

Pred. No.:	8,64e-88	Length:	3808
Score:	1432.00	Matches:	268
Percent Similarity:	98.53%	Conservative:	1
Best Local Similarity:	98.17%	Mismatches:	3
Query Match:	97.08%	Indels:	1
DB:	22	Gaps:	0

US-10-047-021-86\_COPY\_28\_303 (1-276) x AAS01695 (1-3808)

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Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 183 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCAGGACCAGCTGTTCCAGGCCCTGSC 242
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 243 CCTGCCAGGATGAGCTGCCAAGCCTCAGGCCAGCCACCTCCACCATCCGCTGGTTGCTG 302
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 303 AATGGGACGCCCTCGAGCATGTGTCGCCCCAGACCACACACCTCTCGCTGATGGGACC 362
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 363 CTTCTGTGCTACAGCCCTCGCCGGGGACATGCCCCACGATGGCCAGGCCCTGTCCACA 422
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 423 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCCGAGTCAGCAGAGGC 482
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 483 GCTCGGCTGTCTGTGGCTGTCTCCGGAGGATTTCCAGATCCAGCCCTCGGGACATGGTG 542
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140
Db 543 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCCTCGGGCCACCAGAGCCC 602
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 603 ACAGTCTCATGTGTGGAAGATGGGAAACCCCTCGGCCCTCCAGCCCGGAAGGCACACAGTG 662
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Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCys 180  
Dd TCCGGGGGTCCTCTGCTGATGCAAGACAGAGAAGAGTGAAGAGGACCTACATGTGT 722  
Qy 181 ValAlaThrAnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
Dd GTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCGGGTTTCCATCCAGGAG 782  
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220  
Dd TCCGGGGGTCCTCTGCTGATGCAAGACAGAGAAGAGTGAAGAGGACCTACATGTGT 722  
Qy 221 ThrLeuLeuAnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\* 240  
Dd ACATGCTGAACCCGGATCTTCGAGAGCGGCGCTGCGCAATCTTACAGCGGCTTGTTCAGGACCCAG 962  
Qy 241 TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260  
Dd TGAAGAGTCAAGTGGCCCTGCTGCGCTGCGCAATCTTACAGCGGCTTGTTCAGGACCCAG 962  
Qy 260 GLeuProArgGluAlaArgGluLeuLeuArgGlyGlnArg 272  
Dd ACTGCGCGGAGCGCAGGAGCTCCGTTGGGCGAGG 999

## RESULT 9

AAH18180  
ID AAH18180 standard; cDNA; 4262 BP.  
AC AAH18180;  
DT 26-JUN-2001 (first entry)  
DE Human cDNA sequence SEQ ID NO:18084.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PF 28-JUL-2000; 2000EP-0116126.  
PR 29-JUL-1999; 95JP-0248036.  
PR 27-AUG-1999; 95JP-0300253.  
PR 11-JAN-2000; 2000JP-0118776.  
PR 02-MAY-2000; 2000JP-0183767.  
PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602  
PT full-length cDNAs defined in the specification, and for the detection  
PT and/or diagnosis of the abnormality of the proteins encoded by the  
PT full-length cDNAs.

XX Claim 8; SEQ ID 18084; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

XX Sequence 4262 BP; 873 A; 1333 C; 1209 G; 847 T; 0 other;

## Alignment Scores:

Pred. No.: 3.38e-87 Length: 4262  
Score: 1424.00 Matches: 267  
Percent Similarity: 98.17% Conservative: 1  
Best Local Similarity: 97.80% Mismatches: 4  
Query Match: 96.54% Indels: 1  
DB: 22 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x AAH18180 (1-4262)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Dd 121 CAGGACTCCCGCGCCAGATCCTAGTCCACCCCGAGGACGAGCTGTTCCAGGGCCCTGGC 180  
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
Dd 181 CTGCGCAGATGAGCTGCCAAGCTCAGGCGCAGCCACTCCACCATCCGCTGTGTG 240  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Dd 241 AATGGCGAGCCCTGAGCATGTGTCGCCAGAGCCACACACCATCTCTCTGTATGGGACC 300  
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Dd 301 CTCTGTCTGTACAGCCCCCTGCCCGGGGACATGCCCCAGATGGCCAGGCTGTCCACA 360  
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Dd 361 GACCTGGGTGTCTACACATGTGAGGCCAGCACACCGGCTGGCAGCGCAGTCAGCAGAGC 420  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Dd 421 GCTCGGCTGTCTGTGTGCTGCTCCTCGGGAGGATTTCCAGATCCAGACCATGCTG 480  
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140  
Dd 481 GCTGTGTGTGTGTGAGCAGTCTTACTCTGGAATGTGGCGCCCTGGGGCCACCCAGAGCCC 540  
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160  
Dd 541 ACAGTCTCATGTGTGGAAGATGAGAAACCCCTGGCCCTCCAGCCCGGAGGACACACATG 600  
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCys 180  
Dd 601 TCCGGGGGGTCCCTGTCTGTGTGTCGCAAGAGACAGAGAAGAGTGCAGGAGGACCTACATGTGT 660  
Qy 181 ValAlaThrAnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
Dd 661 GTGGCCACCAACAGCGCAGGACACAGGAGAGCGCGCGCGGCTTCCATCCAGGAG 720  
Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220  
Dd 721 CCCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGTGGAAATCTG 780  
Qy 221 ThrLeuLeuAnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu\*\*\* 240  
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DB:	22	Gaps:	0
US-10-047-021-86_COPY_28_303 (1-276) x AAH78073 (1-4262)			
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Db	181	CCTGCCAGGATGAGCTGCAAGCCTCAGSCCAGCCACCTCCACCATCCGCTGGTGGCTG	240
Qy	41	AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr	60
Db	241	AATGGGAGGCCCTTGAGCATGGTGGCCCCAGACCCACACCCTCTCTGCTGATGGGACC	300
Qy	61	LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr	80
Db	301	CTTCTGTGCTACAGCCCTTGCCTGGGGGACATGCCACGATGGCCAGGCCCTGTCCACA	360
Qy	81	AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly	100
Db	361	GACCTGGGTGTCATACATGTGAGGCCAGCAACCGGCTTGGCACCAGCAGTCAGCAGAGGC	420
Qy	101	AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal	120
Db	421	GCTCGGCTGCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGACAGCATGGTG	480
Qy	121	AlaValValGlyGluGlnPheThrLeuGluCysGlyProProProTyrGlyHisProGluPro	140
Db	481	GCTGTGGTGGGTGAGCAGTTTACTCTTGGAAATGTGGCGCGCCCTGGGGCCACCACGAGGCC	540
Qy	141	ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal	160
Db	541	ACATGCTCATGGTGGAAAGATGAGAAACCCCTTGGCCCTCCAGCCCGGAAGGCACACAGTG	600
Qy	161	SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys	180
Db	601	TCCGGGGGTCCCTGCTGATGGCAAGACAGAGAGAGAGTGACCAAGGGGACCTTACATGTGT	660
Qy	181	ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu	200
Db	661	GTGGCCACCAACAGCGCAGGACACAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAG	720
Qy	201	ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAenVal	220
Db	721	CCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGGAAATGTG	780
Qy	221	ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu**	240
Db	781	ACACTGTGTAACCCGGATCTCTGCGAGAGGGCCCAAGCCTAGACCGCGCGTGTGGCTCAGC	840
Qy	241	TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr	260
Db	841	TGGAAAGTTCAGTGGCCCTGTCTGGCCTGCCCAATCTTACAGGCCCTTGTTCAGGACCCAG	900
Qy	260	gLeuProArgGluAlaArgGluLeuArgGlyGlnArg	272
Db	901	ACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG	937

AAH78073	
ID	AAH78073 standard; DNA; 4262 BP.
XX	
XX	
AC	AAH78073;
XX	
XX	
DT	26-NOV-2001 (first entry)
XX	
XX	
XX	Nucleotide sequence of a human protein kinase/protein phosphatase.
KW	Human; protein kinase; protein phosphatase; signal transduction;
KW	intracellular signalling pathway; ss.
XX	
OS	Homo sapiens.

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40..2418
/*tag= a
/product= "protein kinase/protein phosphatase"

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XX	08-FEB-2001.	XX
PD		XX
XX		XX
XX	28-JUL-2000; 2000WO-JP05060.	XX
XX		XX
PR	29-JUL-1999; 99JP-0248036.	XX
PR	18-OCT-1999; 99US-0159590.	XX
PR	11-JAN-2000; 2000JP-0118776.	XX
PR	17-FEB-2000; 2000US-0183322.	XX
PR	02-MAY-2000; 2000JP-0183767.	XX
XX		XX
PA	(HELI-) HELIX RES INST.	PA

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;  
Senoo C, Nezu J;  
WPI; 2001-564736/63.  
P-PSDB; AAG67430.  
XX  
DR  
DR

The present sequence encodes a human protein kinase/protein  
 phosphatase. The polypeptides are expected to participate  
 in transduction in cells. The kinase phosphatases are connected  
 intracellular signalling pathways. Antisense oligonucleotides  
 compounds identified by screening (agonists or antagonists)  
 used to treat human or animal disorders associated with  
 function of the protein. In addition, the polypeptides  
 as target molecules for drug development.

Sequence 4262 BP: 873 A; 1333 C; 1209 G; 847 T; 0 other:

Pred. No.:	3.38e-87	Length:	4362
Score:	1424.00	Matches:	267
Percent Similarity:	98.17%	Conservative:	1
Best Local Similarity:	97.80%	Mismatches:	4
Query Match:	96.54%	Indels:	1

cell proliferative disorder; neurological disorder; Alzheimer's disease.

XX Homo sapiens.

XX Key Location/Qualifiers  
CDS 2..2806

FT /\*tag= a

FT /partial

FT /product= "TANGO 330 form 1 protein"

FT /note= "The ORF is specifically claimed. This sequence

FT lacks a start codon"

FT variation

FT replace (4,C)

FT /\*tag= b

FT variation

FT replace (5,T)

FT /\*tag= c

FT variation

FT replace (9,T)

FT /\*tag= d

FT variation

FT replace (159,A)

FT /\*tag= e

XX WO200123523-A2.

XX 05-APR-2001.

XX 02-OCT-2000; 2000WO-US27202.

XX 30-SEP-1999; 99US-0409634.

XX (MILL-) MILLENNIUM PHARM INC.

XX KIRST S, WRIGHTON N, FRASER CC;

XX WPI; 2001-235372/24.

XX P-PSDB; AAU00500.

PT Isolated secreted proteins and their encoding nucleic acids are used  
PT for diagnosis and treatment of e.g. bacterial and viral infections,  
PT autoimmune diseases and inflammatory disorders -

XX Claim 2; Fig 13; 261pp; English.

XX The present sequence encoding for human TANGO 330 form 1 is  
XX isolated from cDNA clone jthAa060g22 from a human adrenal gland  
XX cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins  
XX which also includes TANGO 315 (AAU00498-AAU00499); TANGO 437 (AAU00502)  
XX and TANGO 480 (AAU00503). The nucleic acids encoding these proteins  
XX are useful as modulating agents in regulating a variety of cellular  
XX processes and can be used to express the proteins in a host cell in  
XX gene therapy applications. Antisense nucleic acid molecules and  
XX expression vectors containing the TANGO nucleic acids are also described.  
XX Diagnostic assays can be used to detect genetic alterations in the TANGO  
XX nucleic acids and to identify compounds that bind to or modulate activity  
XX of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to  
XX monitor protein levels in tissue as a clinical testing procedure.  
XX TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids  
XX and proteins may be used to diagnose, treat and monitor disorders of the  
XX adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They  
XX can also be used to treat cell proliferative disorders (e.g. cancer),  
XX and neurological disorders e.g. Alzheimer's disease.

XX Sequence 3042 BP; 607 A; 1008 C; 859 G; 568 T; 0 other;

Alignment Scores:

Pred. No.: 7.25e-64 Length: 3042  
Score: 1077.00 Matches: 207  
Percent Similarity: 97.20% Conservative: 1  
Best Local Similarity: 96.73% Mismatches: 4  
Query Match: 73.02% Indels: 2  
DB: 22 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x AAS01694 (1-3042)

QY 61 LeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisaspGlyGlnAlaLeuSerTh 80

Db	43	CTCTGCTCATGTCGCCCCCTGCGGGGACATGCCACAGTGGCCAGCCCTGTCCAC	102
Qy	80	rAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgG1	100
Db	103	AGACCTGGGTGTCTACACATGTGAGCCAGCAACCGGCTTGGCAGCGCAGTCAGCAGG	162
Qy	100	YAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVa	120
Db	163	CGCTGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGGCTCGGACATGGT	222
Qy	120	lAlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPr	140
Db	223	GGCTGTGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGCGCCAGAGCC	282
Qy	140	oThrValSerTrpTrpIysaspGlyIysProLeuAlaLeuGlnProGlyArgHisThrVa	160
Db	283	CACAGTCTCATGTGTGGAAGATGGAAACCCCTGGCCCTCAGCCCGGAAGGCACAGT	342
Qy	160	lSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**ThrTyrMetCy	180
Db	343	GTCCGGGGGTCCCTGCTGATGGCAGAGCAGAGAGTGACGAAGGGACCTACATGTG	402
Qy	180	sValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnG1	200
Db	403	TGTGGCCACCAACAGCGCAGACATAGGAGAGCGCGCAGCGCGGTTCCTCATCCAGGA	462
Qy	200	uProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVa	220
Db	463	GCCCCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGGAAAATGT	522
Qy	220	lThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu**	240
Db	523	GACACTGCTGAACCCGATCTTCGAGAGGGCCCCCAGCCTAGACCGCGGCTGTGGCTCAG	582
Qy	240	*TrpLysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGlyProA	260
Db	583	CTGGAAGTCACTGGCCCTGCTGCGCTGCCCAATCTTACACGGCCTTGTTCAGGCCCA	642
Qy	260	rgLeuProArgGluAlaArgGluLeuArgGlyGlnArg	272
Db	643	GACTGCCCGGAGCGCCAGGAGCTCGTGGCAGAGG	680
RESULT 12			
Db	ABK87138		
ID	ABK87138	standard; cDNA; 3688 BP.	
XX	AC	ABK87138;	
XX	DT	07-OCT-2002 (first entry)	
XX	DE	cDNA mouse ECSM4 protein.	
XX	KW	Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculture;	
XX	KW	imaging vascular endothelium; proliferative disease; cancer;	
XX	KW	psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;	
XX	KW	endothelial damage; tumour neovasculture; cardiac disease;	
XX	KW	endometriosis; hypoxic condition; angiogenesis; cytostatic;	
XX	KW	cardiant; gene; ss.	
XX	OS	Mus sp.	
XX	PH	Key Location/Qualifiers	
FT	CDS	6..3053	
FT	FT	/*tag= a	
FT	FT	/note= "ECSM4 #1"	
FT	CDS	3393..3512	
FT	FT	/*tag= b	
FT	FT	/note= "ECSM4 #2"	
FT	CDS	3579..3683	
FT	FT	/*tag= c	
FT	FT	/note= "ECSM4 #3"	
XX	XX		

```
PN WO200236771-A2.
XX PD 10-MAY-2002.
XX PF 06-NOV-2001; 2001WO-GB04906.
XX PR 06-NOV-2000; 2000US-245566P.
XX PR 07-MAR-2001; 2001US-273662P.
XX PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX PI Bicknell R, Huminiecki L;
XX DR WPI; 2002-508120/54.
XX DR P-PSDB; AAU99420, AAU99421, AAU99422.
XX PT Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes
XX PS Disclosure; Fig 13; 248pp; English.
XX CC The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
CC proteins are useful for imaging vascular endothelium in the body of
CC an individual, and for diagnosing and treating a proliferative
CC disease or condition involving the vascular endothelium (preferably,
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in
CC the manufacture of diagnostic or prognostic agent for such conditions.
CC The proteins are also useful for detecting endothelial damage or
CC activation, detecting a tumour or tumour neovasculature, cardiac
CC disease, or endometriosis by detecting the amount of ECSM4 present in
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in
CC gene therapy for treating a hypoxic condition such as cancer, cardiac
CC disease, endometriosis or atherosclerosis and in the manufacture of
CC medicaments for treating the above disease. The sequences are useful
CC for modulating angiogenesis in an individual. The present sequence
CC encodes mouse ECSM4 protein.
XX SQ Sequence 3688 BP; 801 A; 1115 C; 1011 G; 761 T; 0 other;

Alignment Scores:
Pred. No.: 8,49e-63 Length: 3688
Score: 1062.50 Matches: 204
Percent Similarity: 83.52% Conservative: 24
Best Local Similarity: 74.73% Mismatches: 43
Query Match: 72.03% Indels: 2
DB: 24 Gaps: 1

US-10-047-021-86_COPY_28_303 (1-276) x ABR07138 (1-3688)
QY 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
DB 120 GATTCTCCACCCAGATCTAGTTCACCCAGGACCACTACTTCAGGGCTCTGGCCCA 179
QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuAsn 41
DB 180 GCCAAGATGAGTGCAGATCATCCCGGCCCAACCACTCCCACTATCCGCTGGCTGTAAT 239
QY 42 GlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeu 61
DB 240 GGGCAGCCCTCAGCATGCGCCACCCAGACCTACATTACCTTTTCCGGATGGGACCTC 299
QY 62 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThr 80
DB 300 CTGTTACATCGGCCCTCTGTCAGGACGCGCCACAAGATGACCAAGAACATCTCTCAGCA 359
QY 81 AspLeuGlyValIleThrCysGlnAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
DB 360 ATCCCTGGGTGTACACATGTGAGGCCAGCAACCGGCTGGGCACAGCATGTAGCCGGGT 419
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120

Db 420 GCTAGGCTGTCTGTGGCTGTCTTCCAGGAGGACTTCCAGATCCCAACCTCGGACACAGTG 479
QY 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
DB 480 GCCGTGGTGGGAGAGAGCTTGGTCTTTCAGTGTGTGCTCTCCCTGGGGCTACCCAAAACCC 539
QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
DB 540 TCGGTCTCATGTGGAGAGACGGGAACCCCTGGTCTCCAGCCAGGAGGCGCACAGTA 599
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTrpMetCys 180
DB 600 TCTGGGATTCCTGATGCTGCAAGAGCAGAGAAGATGACTCGGGGACCTATATGTGT 659
QY 181 VallalaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
DB 660 ATGGCCACCAACAATGCTGGGCAACGGAGAGCCGAGCAGCGGCTGTATCCAGGAA 719
QY 201 ProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
DB 720 TCCAGGACCACAGGAACATCTAGAGCTTCTGGCTGTTCGATTCAGCTGGAAAATGTG 779
QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu** 240
DB 780 ACCCTGCTAAACCCGCAACCTGTAAGAGTCCCAAGCCTCGGCCCATCCGTGTGGCTCAGC 839
QY 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
DB 840 TGGAAGGTGAGCGGCCCTGCTGCACCTCTCGATCATACACAGCTCTGTTTCCAGGACTCAG 899
QY 260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
DB 900 AGGTCCCCCAGGACCAGGATCTCCATGGACAGAGG 936

RESULT 13
AAH08234
ID AAH08234 standard; cDNA; 756 BP.
XX AC AAH08234;
XX DT 26-JUN-2001 (first entry)
XX DE Human cDNA clone (5'-primer) SEQ ID NO:5069.
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX OS Homo sapiens.
XX PN EP1074617-A2.
XX PD 07-FEB-2001.
XX PF 28-JUL-2000; 2000EP-0116126.
XX PR 29-JUL-1999; 95JP-0248036.
XX PR 27-AUG-1999; 95JP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX DR WPI; 2001-318749/34.
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
XX PT full-length cDNAs defined in the specification, and for the detection
XX PT and/or diagnosis of the abnormality of the proteins encoded by the
XX PT full-length cDNAs -
```

PS Claim 1; SEQ ID 5069; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

SQ Sequence 756 BP; 147 A; 242 C; 236 G; 128 T; 3 other;

#### Alignment Scores:

Pred. No.: 3.81e-63 Length: 756  
Score: 1057.00 Matches: 205  
Percent Similarity: 97.17% Conservative: 1  
Best Local Similarity: 96.70% Mismatches: 6  
Query Match: 71.66% Indels: 2  
DB: 22 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x AAH08234 (1-756)

Qy 1 GlnAspSerProGlnIleValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db 121 CAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACCGCTTCCAGGGCCCTGGC 180  
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
Db 181 CCTGCCAGATGAGTGCAGAGCTCAGCCAGCCACCTCCACCATCCGCTGGTGTG 240  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisLeuLeuProAspGlyThr 60  
Db 241 AATGGCAGCCCTGAGCATGGTGGCCCGCCAGACCCACACCATCTCTGCTGTATGGGACC 300  
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db 301 CTCTGTCTGTACAGCCCTCCCGGGGAGATGCCACAGATGGCCAGCCCTGTCCACA 360  
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db 361 GACCTGGTGTCTACATGTGAGCCAGCAACCGCTTGCACGGCAGTCCAGCAGAGGC 420  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db 421 GCTCGGTGTCTGTGGTGTCTCTCGGAGGAGTATTCAGATCCAGCCCTCGAGACATGGTG 480  
Qy 121 AlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140  
Db 481 GCTGTGGTGGTGTAGACATTTACTCTGAATGTGGCGCCCTCGGGGCCACCCAGAGCCC 540  
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160  
Db 541 ACAGTCTCATGTTGAAGATGAGAAACCCCTTGGCCCTCCAGCCCGGAGGACACACAGTG 600  
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyMetCys 180  
Db 601 TCCGGGGGGTCTCTGCTGATGGCAAGAGAGAGTGTGACGAAGGAGCCTACATGTGT 660

Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200  
Db 661 GTGGC-ACCACACAGCGCAGACACACAGGAGAGCGGCGACCC-CGGGTTTCATTCAGAG 718  
Qy 201 ProGlnAspTyrThrGluProValGluLeuAla 212  
Db 719 CCCGANGACTACACGGAACCTGTGGAACCTTTGGCT 754

#### RESULT 14

AAV69278  
ID AAV69278 standard; cDNA; 4291 BP.  
AC AAV69278;  
XX 01-MAR-1999 (first entry)  
DT Human T85 cDNA.  
DE T85; FMHB-6D4; FMHV-SD4; human; neurological disorder; therapy;  
KW diagnosis; ss.  
XX Homo sapiens.  
OS

Key Location/Qualifiers

FT CDS 958..3219

FT sig\_peptide 958..1017

FT mat\_peptide 1018..3216

FT WO9848051-A2.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-US07714.

XX 10-OCT-1997; 97US-0062017.

XX 18-APR-1997; 97US-0044746.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Holtzman D, McCarthy SA;

XX WPI; 1999-024021/02.

XX P-PSDB; AAW83927.

XX New isolated human FTHMA-070 and T85 proteins - used to develop  
XX products for the diagnosis and therapy of disorders involving  
XX cellular processes, e.g. neuronal development.  
XX Claim 24; Fig 3; 127pp; English.

XX This claimed cDNA sequence, the coding region of which is also  
XX claimed, codes for novel human T85 (see AAW83927), also referred to  
XX FMHB-6D4 and FMHB-SD4. The cDNA was identified in a human foetal  
XX brain cDNA library using a screen designed to identify genes  
XX encoding proteins having a functional signal sequence. T85 nucleic  
XX acids and polypeptides of the invention are useful as modulating  
XX agents in regulating a variety of cellular processes. They can be  
XX used for identifying compounds which bind to or modulate the  
XX activity of the polypeptides (claimed). They can also be used in  
XX screening assays, detection assays (e.g. chromosomal mapping,  
XX tissue typing, forensic biology), predictive medicine (e.g.  
XX diagnostic assays, prognostic assays, monitoring clinical trials,  
XX and pharmacogenomics), and methods of treatment (e.g. therapeutic  
XX and prophylactic) e.g. for neurological disorders.

XX SQ Sequence 4291 BP; 1154 A; 1011 C; 1045 G; 1081 T; 0 other;

Alignment Scores:

Pred. No.: 4.87e-21 Length: 4291

Score: 446.50 Matches: 91

Percent Similarity: 55.96% Conservative: 31  
 Best Local Similarity: 41.74% Mismatches: 87  
 Query Match: 30.27% Indels: 9  
 DB: 20 Gaps: 2

US-10-047-021-86\_COPY\_28\_303 (1-276) x AAV69278 (1-4291)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
 Db 1030 GAAGATTTTCACCTCGCATTTGTTGAACACCCCTTCAGACCTGATTTCTCAAAAGAGAA 1089

Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
 Db 1090 CCTGCAACTTTGAACCTGAAGCGCGCCACACCCACTTAAATGGTACAAA 1149

Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHis 57  
 Db 1150 GGGGAGAGAGAGTGGAGACAGACAAAGATGACCTCGTCACCCGATTTGTGCGCG 1209

Qy 58 AspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAla 77  
 Db 1210 AGTGGATCTTTATTTTCTTACCT-----ATAGTACATGAGCGGAAA 1251

Qy 78 LeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaVal 97  
 Db 1252 AGTAGACCTGATGAAGAGTCTATGCTGTGTAGCAAGAAATTTACCTTCGAGAGCTGTG 1311

Qy 98 SerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArg 117  
 Db 1312 AGCCACANTCATCGCTGGAGTAGGCATCTCTCGGATGACTTCAGACAAACCTTCG 1371

Qy 118 AspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHis 137  
 Db 1372 GATGTCATGCTTCAGTAGGAGAGCTGCAGTAATGTAATGCAACCTCCACGAGGCCAT 1431

Qy 138 ProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArg 157  
 Db 1432 CCTGAGCCCACTTTTCATGGAAGAAGATGGCTCTCCACTGATGATAAAGATGAAAGA 1491

Qy 158 HisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*Thr 177  
 Db 1492 ATAACTATACGAGAGGAAGCTCATGATCACTTACACCCGTAAGAAGTCCGCTGGCAA 1551

Qy 178 TyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSer 197  
 Db 1552 TATGTTGTGTTGTTACCAATATGTTGGGAACGTGAGAGTGAAGTACCGAGCTGACT 1611

Qy 198 IleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIle 215  
 Db 1612 GTCTTAGAGAGACCATCATTTGTTGAAGAGACCCAGTAACTTGGCAGTAACCTGTG 1665

RESULT 15  
 AAX55770  
 ID AAX55770 standard; cdna; 4956 BP.  
 AC AAX55770;  
 XX AAX55770;  
 XX 30-JUL-1999 (first entry)  
 XX Human Robo 1 polypeptide encoding cDNA.  
 DE Comm polypeptide; Robo polypeptide; commissureless; roundabout;  
 KW modulation; nerve cell function; ds.  
 XX Homo sapiens.  
 OS WO9925833-A1.  
 FN 27-MAY-1999.  
 XX 13-NOV-1998; 98WO-024327.  
 XX 14-NOV-1997; 97US-0065543.  
 XX

(REGC ) UNIV CALIFORNIA.  
 Goodman C, Kid T, Mitchell KJ, Russell C, Tear G;  
 WPI; 1999-338008/28.  
 P-PSDB; AAY13566.  
 Modulation of Robo-Comm polypeptide interactions  
 Disclosure; Page 42-44; 56pp; English.  
 The invention relates to a method for modulating the amount of Comm (commissureless) polypeptide in contact with a cell expressing active Robo (roundabout) on its surface. The method comprises modulating the effective amount of Comm polypeptide in contact with the cell, where the amount of expressed active Robo is specifically modulated inversely with the modulation of the effective amount of Comm in contact with the cell. The method is used to modulate the amount of active Robo expressed on a cell. The method can be used to screen for agents that modulate Robo:Comm interactions. This is particularly useful for modulating nerve cell function.

Sequence 4956 BP; 1480 A; 1230 C; 1186 G; 1060 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 5.67e-21 Length: 4956  
 Score: 446.50 Matches: 91  
 Percent Similarity: 55.96% Conservative: 31  
 Best Local Similarity: 41.74% Mismatches: 87  
 Query Match: 30.27% Indels: 9  
 DB: 20 Gaps: 2

US-10-047-021-86\_COPY\_28\_303 (1-276) x AAX55770 (1-4956)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
 Db 190 GAAGATTTTCACCTCGCATTTGTTGAACACCCCTTCAGACCTGATTTCTCAAAAGAGAA 249

Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40  
 Db 250 CCTGCAACTTTGAACCTGAAGCGCGCCACACCCACTTAAATGGTACAAA 309

Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHis 57  
 Db 310 GGGGAGAGAGAGTGGAGACAGACAAAGATGACCTCGCTCACACCGAATTTGTGCGCG 369

Qy 58 AspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAla 77  
 Db 370 AGTGGATCTTTATTTTCTTACCT-----ATAGTACATGAGCGGAAA 411

Qy 78 LeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaVal 97  
 Db 412 AGTAGACCTGATGAAGAGTCTATGCTGTGTAGCAAGAAATTTACCTTCGAGAGCTGTG 471

Qy 98 SerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArg 117  
 Db 472 AGCCACAATCATCGCTGGAAAGTAGCCATCTTCGGGATGACTTCAGACAAACCCCTCG 531

Qy 118 AspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHis 137  
 Db 532 GATGTCATGTTGTCAGTAGGAGAGCTTCAGTAATGTAATGCAACCTCCACGAGGCCAT 591

Qy 138 ProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArg 157  
 Db 592 CCTGAGCCCACTTTTCATGGAAGAAGATGGCTCTCCACTGGATGATAAAGATGAAGA 651

Qy 158 HisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*Thr 177  
 Db 652 ATAACTATACGAGAGGAAGCTCATGATCACTTACACCCGTAAGAAGTACCGCTGCAA 711

Qy 178 TyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSer 197  
 Db 97US-0065543.

Db 712 TATGTTTGTGTTGTTACCAATATGTTGGGGAACGTCAGAGTGAAGTAGCCGAGCTGACT 771  
Qy 198 IleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIle 215  
Db 772 GTCTTAGAGAGACCATCATTTTGTGAAGAGAGACCCAGTAACTTGGCAGTAACTGTG 825

Search completed: January 31, 2004, 12:48:19  
Job time : 231.228 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2004, 12:35:25 ; Search time 60.5389 Seconds  
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2012.290 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303

Perfect score: 1475

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Scoring table:

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*  
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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	276.5	18.7	6814	US-09-484-970B-66
2	218.5	14.8	5690	Sequence 66, Appli
3	218.5	14.8	5690	Sequence 2, Appli
4	206.5	14.0	4078	US-08-716-679-2
5	206.5	14.0	6000	US-09-016-434-1132
6	206.5	14.0	6000	US-08-348-006B-6
7	206.5	14.0	6000	US-08-800-825A-6
8	206.5	14.0	6000	US-09-158-657-6
9	206	14.0	6000	PCT-US94-10166-6
10	206	14.0	3888	US-08-506-296B-13
11	206	14.0	4608	US-09-041-886-24
12	199	13.5	1426	PCT-US94-05277-1
				US-09-638-649-2

13	198	13.4	1042	2	US-08-427-497E-6	Sequence 6, Appli
14	198	13.4	3774	2	US-08-341-843B-1	Sequence 1, Appli
15	198	13.4	3774	2	US-08-427-497E-1	Sequence 2, Appli
16	198	13.4	3774	2	US-08-427-497E-2	Sequence 2, Appli
17	194.5	13.2	3943	4	US-08-506-296B-27	Sequence 27, Appli
18	192	13.0	3189	2	US-08-427-497E-3	Sequence 3, Appli
19	191.5	13.0	4078	4	US-09-016-434-1120	Sequence 1120, Ap
20	191	12.9	3783	4	US-08-506-296B-20	Sequence 20, Appli
21	189	12.8	3398	5	PCT-US95-08493-12	Sequence 12, Appli
22	189	12.8	4843	3	US-08-986-485-1	Sequence 1, Appli
23	185.5	12.6	1391	4	US-09-638-649-4	Sequence 4, Appli
24	182.5	12.4	5824	4	US-08-620-312D-72	Sequence 72, Appli
25	177.5	12.0	3551	4	US-09-620-312D-760	Sequence 760, App
26	176	11.9	3991	4	US-08-506-296B-3	Sequence 3, Appli
27	175.5	11.9	1493	2	US-08-752-307B-6	Sequence 6, Appli
28	175.5	11.9	1493	4	US-09-707-802-6	Sequence 6, Appli
29	175.5	11.9	1493	4	US-09-991-326-6	Sequence 6, Appli
30	172	11.7	957	2	US-08-633-148-3	Sequence 3, Appli
31	172	11.7	1023	2	US-08-633-148-1	Sequence 1, Appli
32	170.5	11.6	3360	1	US-08-408-093-5	Sequence 5, Appli
33	170.5	11.6	3360	1	US-08-408-420A-5	Sequence 5, Appli
34	170.5	11.6	3360	1	US-08-714-901-5	Sequence 5, Appli
35	170.5	11.6	3360	3	US-08-040-741-5	Sequence 5, Appli
36	165.5	11.2	2610	1	US-08-374-834-17	Sequence 17, Appli
37	165.5	11.2	2610	1	US-08-644-271-28	Sequence 28, Appli
38	165.5	11.2	2610	4	US-09-077-955-32	Sequence 32, Appli
39	165	11.2	2869	1	US-08-374-834-2	Sequence 2, Appli
40	165	11.2	2869	1	US-08-644-271-2	Sequence 2, Appli
41	165	11.2	2869	4	US-09-077-955-2	Sequence 2, Appli
42	163.5	11.1	3453	4	US-08-877-730-7	Sequence 7, Appli
43	162.5	11.0	1143	4	US-09-877-730-3	Sequence 3, Appli
44	162.5	11.0	2715	4	US-09-877-730-5	Sequence 5, Appli
45	162.5	11.0	2958	4	US-09-877-730-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-484-970B-66  
; Sequence 66, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmut, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 66  
; LENGTH: 6814  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 199882.3  
; NAME/KEY: unsure  
; LOCATION: 1838, 5528  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-66

Alignment Scores:			
Pred. No.:	1.4e-13	Length:	6814
Score:	276.50	Matches:	93
Percent Similarity:	38.80%	Conservative:	30
Best Local Similarity:	29.34%	Mismatches:	125
Query Match:	18.75%	Indels:	69
DB:	4	Gaps:	11

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-09-484-970B-66 (1-6814)



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Db |||||
Oy 790 CCGCGATCACTCCGAGCCCGAGGACGACATGTGACCTCGGGAAACACCGTGTACTTC 849
Db |||||
Oy 25 SerCysArgAlaSerGlyGlnProProProProThrLeuArgTrpLeuLeuAsnGlyGlnPro 44
Db |||||
Oy 850 ACCTGCAGACCGGAAGGCAACCCCAAGCCTGAGATCATCTGCTCGGAAACAATAATGAG 909
Db |||||
Oy 45 LeuSerMetValProProAspProHisHisLeuLeuProAspGlyThrLeuLeuLeu 64
Db |||||
Oy 910 CTGAGCATGAAGACAGATCCCGCTAACTTGTGGACGATGGAGCCCTGATATC--- 966
Db |||||
Oy 65 GlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyVal 84
Db |||||
Oy 967 -----CAGAACACACAGGAGACAGACCGGGTATC 996
Db |||||
Oy 85 TyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSer 104
Db |||||
Oy 997 TACCAGTCATGGCAAGACGCTGGCCGAGAGGTGAAGACGCAAGAGGTGACCTCAGG 1056
Db |||||
Oy 105 Val-----AlaValLeuArgGluAspPheGlnLeuGlnProArgAspMetValAlaVal 122
Db |||||
Oy 1057 TACTTCGGGTCTCCAGCTGCACCCACTTTTGTATCCAGCCACACAGATACAGAGGTGCTG 1116
Db |||||
Oy 123 ValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrVal 142
Db |||||
Oy 1117 GTTGGGAGAGGTCACGCTGAGGTGACGCCCA---GGCCACCCCGCCCGGATC 1173
Db |||||
Oy 143 SerTrpTrpLys---AspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSer 161
Db |||||
Oy 1174 TCCTGGACGAGAGGTGACCGCACACCTTCGACGTGACCGCGGGTGAACATCACGCGCT 1233
Db |||||
Oy 162 GlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysVal 181
Db |||||
Oy 1234 TCTGGCGGGCTTACATACAGAACCTGTCAGAGGGGGACACGGAGAGATGCGTGCTCT 1293
Db |||||
Oy 182 AlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluPro 201
Db |||||
Oy 1294 GCGACCAACATGACAGGCTCATCCACCGCTTTCATCATCTGCTCCAGGCTCTCTCT 1353
Db |||||
Oy 202 GlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThr 221
Db |||||
Oy 1354 CAGTTCACCTGTGACGCTCAGAC-----AGAGTCGTTATTGAGGGCCAGACC 1401
Db |||||
Oy 222 Leu-Leu-----AsnProAspProAlaGln 229
Db |||||
Oy 1402 GTGATTTCCAGTGTGAAGCAACCGCGCCGCTCATCGCTGACCAAGGGA 1461
Db |||||
Oy 229 uGly-Pro-----LysProArgProAlaVal----- 237
Db |||||
Oy 1462 GGGAGCCAGCTCTCGTGGACCGGGGACCTGGTCTGTATCGGGNACACTTAGAATC 1521
Db |||||
Oy 238 --TrpLeu**TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys 257
Db |||||
Oy 1522 TCTGGTGTTCCTCCACGACGAGGCGGACGATGACGATGACGAGG-----TGTG 1569
Db |||||
Oy 257 erGlyProArgLeuProArgGluAlaArgGluLeuArgGly----- 270
Db |||||
Oy 1570 AACATCATCGGCTCCCA-----GAAGTCGTGGGCCACCTGACTGTGACGCC 1617
Db |||||
Oy 271 -----GlnArgArgAsnThrGly 276
Db |||||
Oy 1618 AGAGTCAACCCAGCTGTTTGCAGCATTCCTCCAGCGGACACACAGTGA 1664
Db |||||
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## RESULT 2

US-08-447-464-2

; Sequence 2, Application US/08447464

; Patent No. 5840842

; GENERAL INFORMATION:

; APPLICANT: Schlössinger, Joseph

; APPLICANT: Yan, Hai

; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN

; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA

```
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,464
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/130,570
; FILING DATE: 01-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5690 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 833..5338
; US-08-447-464-2
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## Alignment Scores:

Pred. No.:	7.98e-09	Length:	5690
Score:	218.50	Matches:	67
Percent Similarity:	47.93%	Conservative:	37
Best Local Similarity:	30.88%	Mismatches:	74
Query Match:	14.81%	Indels:	39
DB:	2	Gaps:	11

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-08-447-464-2 (1-5690)

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Db |||||
Oy 920 GAAGAGCCACCCAGATTTATCAGAGAGCCCAAGATCAGATTGGTGTGCAGGAGCGGTG 979
Db |||||
Oy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp----- 38
Db |||||
Oy 980 GCCTCTCTCGTGTGCCAGGCCACAGGTGACCTAAGCCAGGTCAGCTGGACCAAGAG 1039
Db |||||
Oy 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 56
Db |||||
Oy 1040 GGCAAGAAAGTGAACATCAGACGCTTTGAGACCATTTGACGAG----- 1087
Db |||||
Oy 57 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
Db |||||
Oy 1088 AGTCGGGGCGCGTGTGAGGATCCAGCCA----- 1117
Db |||||
Oy 77 AlaLeuSerThr-----AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 94
Db |||||
Oy 1118 ---CTTCGGACACCCCGGGATGAGACGTGTACAGTGTGTGGCCACAGACTCGTGGGG 1174
Db |||||
Oy 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle 114
Db |||||
Oy 1175 ---GAGATCAGATTTCATGCGAAGCTCACC-----GTCCTCGAGAGGAC---CAGCTG 1222
Db |||||
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Qy 115 GlnProArgAspMetValAlaValValGlyGluGlnPhe----- 127  
 Db 1223 CCTCTGGCTTCCCAACATTGACATGGGCCCCAGTTGAAGTTGTAGAGGGCACAGC 1282  
 Qy 128 -----ThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 145  
 Db 1283 ACAGCCACCATCTCTGTGCTGCCAGC---GGAAACCTGACCTCTGAGATCACCTGGTTC 1339  
 Qy 146 LysAspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGly 162  
 Db 1340 AAGGACTTCTGCTGTGACCCAGTCCAGCAATGGCGGATCAACAGCAGCTTCGGTCA 1399  
 Qy 163 GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCysValAla 182  
 Db 1400 GGTGCGCTCGAGATTGAGCAGCAGCGAGAGACAGACAGCGGCAAGTACGAGTGTGTGCC 1459  
 Qy 183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGln 199  
 Db 1460 ACCAACAGCGCTGGGGTGGCTACTCATCATCCTGCCAACCTCTACGTGCGA 1510

## RESULT 3

US-08-716-679-2  
 ; Sequence 2, Application US/08716679  
 ; Patent No. 5846800  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlessinger, Joseph  
 ; APPLICANT: Yan, Hai  
 ; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN  
 ; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/716,679  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/130,570  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mirock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 7683-043  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-790-9090  
 ; TELEFAX: 212-869-8864/9741  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5690 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 833..5338

US-08-716-679-2  
 Alignment Scores:  
 Pred. No.: 7,986-09 Length: 5690  
 Score: 218.50 Matches: 67

Percent Similarity: 47.93% Conservative: 37  
 Best Local Similarity: 30.88% Mismatches: 74  
 Query Match: 14.81% Indels: 39  
 DB: 2 Gaps: 11  
 US-10-047-021-86\_COPY\_28\_303 (1-276) x US-08-716-679-2 (1-5690)  
 Qy 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21  
 Db 920 GAAGAGCCACCCAGATTATCAGAGAGCCCAAGATCAGATTGGTGTCTCAGGAGCGGTG 979  
 Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp----- 38  
 Db 980 GCCTCTCTGCTGCTCCAGGCCACAGGTGACCTAAGCCACCGGTGACCTGGAACAAGAAG 1039  
 Qy 39 -----LeuLeuGlnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 56  
 Db 1040 GGCAAGAAAGTGAACCTCACAGCGCTTTGAGACCACTGCTTTGACGAG----- 1087  
 Qy 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76  
 Db 1088 AGCTCGGGCGCTGCTGAGGATCCAGCA----- 1117  
 Qy 77 AlaLeuSerThr-----AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 94  
 Db 1118 ---CTTCGGACACCCCGGATGAGAACGTGTACGAGTGTGTGGCCACAGAACTCGGTGGG 1174  
 Qy 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle 114  
 Db 1175 ---GAGATCAGTTCATGCGAAGCTCACC-----GTCTGCGAGAGGAC---CAGCTG 1222  
 Qy 115 GlnProArgAspMetValAlaValGlyGluGlnPhe----- 127  
 Db 1223 CCTCTGGCTTCCCAACATTGACATGGGCCCCAGTTGAAGTTGTAGAGCGGCACAGC 1282  
 Qy 128 -----ThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 145  
 Db 1283 ACAGCCACCATCTCTGTGCTGCCAGC---GGAAACCTGACCTGAGATCACCTGGTTC 1339  
 Qy 146 LysAspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGly 162  
 Db 1340 AAGGACTTCTGCTGTGAGCCACCCAGTCCAGCAATGGCGGATCAACAGCAGCTTCGGTCA 1399  
 Qy 163 GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCysValAla 182  
 Db 1400 GGTGCGCTCGAGATTGAGCAGCAGCGAGAGACAGACAGCGGCAAGTACGAGTGTGTGCC 1459  
 Qy 183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGln 199  
 Db 1460 ACCAACAGCGCTGGGGTGGCTACTCATCATCCTGCCAACCTCTACGTGCGA 1510

## RESULT 4

US-09-016-434-1132  
 ; Sequence 1132, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2



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Best Local Similarity: 28.82% Mismatches: 94
Query Match: 14.00% Indels: 74
DB: 1 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-08-348-006B-6 (1-6000)

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QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp----- 38
DB 170 GCCTCTTCGTGTGTCAGCCAGGTTGACCCCAAGCCAGGACCTGGAGAACAGAG 229
QY 39 -----LeuLeuAnGlyGlnProLeuSerMetValProAspProHisHisLeuLeu 56
DB 230 GCGAAGAAGGTCAACTCTCAGCGCTTTCAGACGATTGAGTTTGATGAG----- 277
QY 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
DB 278 AGTCAGGGCGGAGTGTGAGGATCCAGCG----- 307
QY 77 AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly 94
DB 308 ---CTGAGGACACCGCGGATGAAACCTGTACGAGTGTGTGCGCCCAAGAACTCGGTGG 364
QY 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
DB 365 ---GAGATCACAGTCATGCCAGCTTACT-----GTCTCCGAGAGGACCACTGCGCC 415
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DB 416 TCTGCTTCCCAACATCGACATGGGCCACAGTTGAAGGTGTGAAGGCGGACGACGACA 475

Alignment Scores:
Pred. No.: 8,63e-08 Length: 6000
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservative: 39
Best Local Similarity: 28.82% Mismatches: 94
Query Match: 14.00% Indels: 74
DB: 2 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-08-800-825A-6 (1-6000)

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DB 110 GAAGAGCCCCCAGGTTTATCAAGAACCCCAAGGACCATCGCGGTGTGCGGGCGGTGTG 169
QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp----- 38
DB 170 GCCTCTTCGTGTGTCAGCCAGGTTGACCCCAAGCCAGGACCTGGAGAACAGAG 229
QY 39 -----LeuLeuAnGlyGlnProLeuSerMetValProAspProHisHisLeuLeu 56
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QY 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
DB 278 AGTCAGGGCGGAGTGTGAGGATCCAGCG----- 307
QY 77 AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly 94
DB 308 ---CTGAGGACACCGCGGATGAAACCTGTACGAGTGTGTGCGCCCAAGAACTCGGTGG 364
QY 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
DB 365 ---GAGATCACAGTCATGCCAGCTTACT-----GTCTCCGAGAGGACCACTGCGCC 415
QY 112 -----PheGlnIleGlnProArgAspMetValAlaValIcGlyGln 126
DB 416 TCTGCTTCCCAACATCGACATGGGCCACAGTTGAAGGTGTGAAGGCGGACGACGACA 475

US-08-800-825A-6
Alignment Scores:
Pred. No.: 8,63e-08 Length: 6000
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservative: 39
Best Local Similarity: 28.82% Mismatches: 94
Query Match: 14.00% Indels: 74
DB: 2 Gaps: 16

US-08-800-825A-6 (1-6000)

QY 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
DB 110 GAAGAGCCCCCAGGTTTATCAAGAACCCCAAGGACCATCGCGGTGTGCGGGCGGTGTG 169
QY 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrp----- 38
DB 170 GCCTCTTCGTGTGTCAGCCAGGTTGACCCCAAGCCAGGACCTGGAGAACAGAG 229
QY 39 -----LeuLeuAnGlyGlnProLeuSerMetValProAspProHisHisLeuLeu 56
DB 230 GCGAAGAAGGTCAACTCTCAGCGCTTTCAGACGATTGAGTTTGATGAG----- 277
QY 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
DB 278 AGTCAGGGCGGAGTGTGAGGATCCAGCG----- 307
QY 77 AlaLeuSerThr-----AspLeuGlyValThrCysGluAlaSerAsnArgLeuGly 94
DB 308 ---CTGAGGACACCGCGGATGAAACCTGTACGAGTGTGTGCGCCCAAGAACTCGGTGG 364
QY 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
DB 365 ---GAGATCACAGTCATGCCAGCTTACT-----GTCTCCGAGAGGACCACTGCGCC 415
QY 112 -----PheGlnIleGlnProArgAspMetValAlaValIcGlyGln 126
DB 416 TCTGCTTCCCAACATCGACATGGGCCACAGTTGAAGGTGTGAAGGCGGACGACGACA 475
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## RESULT 6

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US-08-800-825A-6
; Sequence 6, Application US/08800825A
; Patent No, 5866397
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
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Qy 127 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTyrPlys 146
Db 476 GCCACCATGCTCTGTGCAGCCAGC---GGCAACCTGACCTGAGATCACCCTGTTCAAG 532
Qy 147 AspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGlyGly 163
Db 533 GACTTCCTGCTGTGGATCCTAGTGCCAGCAATGGACGATCAAAACAGCTCGCATCAGGA 592
Qy 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThr 183
Db 593 GCCCTGCAGATTGAAGCAGTGCAGGAACACCGACGAGGCAATATGAGTGTGTGCCACC 652
Qy 184 AsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAsp 203
Db 653 AACAGCGCCGCGTGGC----- 670
Qy 204 TyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeu 223
Db 671 TACTCTCACCTGCCAACCTCTAC---GTGGAGTCCGCGC---CGTGGCCCGCGCTTCTC 726
Qy 224 AsnPro-----AspProAlaGluGlyProLysProArgProAlaValTyrP 238
Db 727 CATCTGCTCCATGAGCCAGAGATCATGCCAGGGGGCAACGTGAACATCA---CTGCGCTGG 785
Qy 239 Leu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys----- 256
Db 786 ---CCGTGG-----GCTCGCCCATGCCATCAG 809

RESULT 7
US-09-158-657-6
; Sequence 6, Application US/09158657
; Patent No. 6214564
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/800,825
; FILING DATE: 14-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18992DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6000 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-158-657-6
Alignment Scores:
Pred. No.: 8,63e-08 Length: 6000
Score: 206.50 Matches: 83
Percent Similarity: 42.36% Conservatives: 39
Best Local Similarity: 28.82% Mismatches: 94
Query Match: 14.00% Indels: 74
DB: 3 Gaps: 16

US-10-047-021-86_COPY_28_303 (1-276) x US-09-158-657-6 (1-6000)
Qy 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21
Db 110 GAAGAGCCCCCAGGTTTATCAAAAGAACCCAGAGCCAGATCGCGGTGTCGGGCGGTG 169
Qy 22 AlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTyrP 38
Db 170 GCCTCTTCTGTGTGTGAGGCGGAGTACCCCAAGCCAGAGTACCTGGAAACAAGAG 229
Qy 39 -----LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 56
Db 230 GGCAAGAGGTCAACTCTAGCGCTTTGAGACGATTGAGTTTGATGAG----- 277
Qy 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76
Db 278 AGTCAGGGGCGAGTGTGAGGATCCAGCG----- 307
Qy 77 AlaLeuSerThr-----AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 94
Db 308 ---CTGAGGACACCGCGGATGAAAGGTAGAGTGTGTGCGCCAGAGATCGGTGGG 364
Qy 95 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAsp----- 111
Db 365 ---GAGATCACAGTCCATGCGGAGTTACT-----GTCTCCGAGAGGAGGACGAGTGC 415
Qy 112 -----PheGlnIleGlnProArgAspMetValAlaValValGlyGluGln 126
Db 416 TCTGGCTTCCCAACATCGACATGCGGCGCCAGATTGAAGGTGTGGAGCGGACACGACA 475
Qy 127 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTyrPlys 146
Db 476 GCCACCATGCTCTGTGCAGCCAGC---GGCAACCTGACCTGAGATCACCCTGTTCAAG 532
Qy 147 AspGlyLysProLeu-----AlaLeuGlnProGlyArg---HisThrValSerGlyGly 163
Db 533 GACTTCCTGCTGTGGATCCTAGTGCCAGCAATGGACGATCAAAACAGCTCGCATCAGGA 592
Qy 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCysValAlaThr 183
Db 593 GCCCTGCAGATTGAAGCAGTGCAGGAACACCGACGAGGCAATATGAGTGTGTGCCACC 652
Qy 184 AsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAsp 203
Db 653 AACAGCGCCGCGTGGC----- 670
Qy 204 TyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeu 223
Db 671 TACTCTCACCTGCCAACCTCTAC---GTGGAGTCCGCGC---CGTGGCCCGCGCTTCTC 726
Qy 224 AsnPro-----AspProAlaGluGlyProLysProArgProAlaValTyrP 238
Db 727 CATCTGCTCCATGAGCCAGAGATCATGCCAGGGGGCAACGTGAACATCA---CTGCGCTGG 785
Qy 239 Leu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCys----- 256
Db 786 ---CCGTGG-----GCTCGCCCATGCCATCAG 809
Qy 257 ---SerGlyProArgLeuProArg 263
```

Db 810 TGAAGTGGATGACGGGGCCGAGG 833

RESULT 8

PCT-US94-10166-6

Sequence 6, Application PC/TUS9410166

GENERAL INFORMATION:

APPLICANT: RODAN, GIDEON A

APPLICANT: SCHMIDT, AZRIEL

APPLICANT: RUTLEDGE, SU JANE

TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSER: JOHN W. WALLEN III

STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.

CITY: RAHWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10166

FILING DATE: 09-SEPT-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/122,032

FILING DATE: 14-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: WALLEN, JOHN W III

REGISTRATION NUMBER: 35403

REFERENCE/DOCKET NUMBER: 18992

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3905

TELEFAX: 908-594-4720

TELEX: 138825

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 6000 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US94-10166-6

Alignment Scores:

Pred. No.: 8 63e-08 Length: 6000

Score: 206.50 Matches: 83

Percent Similarity: 42.36% Conservatives: 39

Best Local Similarity: 28.82% Mismatches: 94

Query Match: 14.00% Indels: 74

DB: 5 Gaps: 16

US-10-047-021-86\_COPY\_28\_303 (1-276) x PCT-US94-10166-6 (1-6000)

Qy 2 AspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGlyPro 21

Db 110 GAAGAGCCCCCAGGTTTATCAAGAAGCCCAAGGACCATGCGCGTGTGCGGGCGTGTG 169

Qy 22 AlaArgMetSerCysArgIleGlnProProProProThrIleArgTTP----- 38

Db 170 GCCTCTTTCTGTGTGTCAGGCGGTCAGGCGGTCAGGCGGTCAGGCGGTCAGGCGGTCAGG 229

Qy 39 -----LeuLeuAspGlnProLeuProLeuSerMetValProProAspProHisLeuLeu 56

Db 230 GGCAAGAAGTCAACTCTCAGCGCTTTGAGACGATTGAGTTTGTATGAG----- 277

Qy 57 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 76

ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 488.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 388 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 12..3773  
US-08-506-296B-13

Alignment Scores:  
Pred. No.: 5,498-08 Length: 3888  
Score: 206.00 Matches: 87  
Percent Similarity: 37.42% Conservative: 35  
Best Local Similarity: 26.69% Mismatches: 106  
Query Match: 13.97% Indels: 98  
Gaps: 4

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-08-506-296B-13 (1-3888)

QY 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db 126 GAACAGTCTCCACGGCGCTGGTCTCTCCACAGATGATC----- 170  
QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTyrLeuLeu 40  
Db 171 -----AGCCTCAAGTGTGAGCGCAGTGGCAAGCCGAAGTGCAGTTCGCTGGACGAGG 224  
QY 41 AenGlyGlnProLeuSerMetValProProProHisHisLeuLeuProAspGlyThr 60  
Db 225 GATGTGTCT-----CACTCAACCCCAAGAGAGAG 254  
QY 61 Leu-----LeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeu 78  
Db 255 CTGGTGTGACGCTGACAGTCCGCGC-----CACTCTGGTCTCTTCCACC 299  
QY 79 SerThrAsp-----LeuGlyValTyrThrCysGluAla 89  
Db 300 ATCAGGGCAACACAGCAACTTTGCTCAGAGTTCCAGGGCATCTACCGCTGCTTTGCC 359  
QY 90 SerAenArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArg 109  
Db 360 AGCAATAGCTGGGACCGCCATGCTCCATGATCCGGCTC-----ATGGCC 407  
QY 110 GlnAspPheGlnLeuProArgAspMetValAlaValVal-----GlyGlu 125  
Db 408 GAGGTGCGCCCAAGTGGCCAAAGAGAGACAGTGAAGCCCGTGGAGTGGAGAGGGGAG 467  
QY 126 GlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTyrTrp 145  
Db 468 TCAGTGGTCTCTGCGCTTGAACCTCC-----CCAAAGTGCAGAGCCTCTCCGGATCTACTGG 524  
QY 146 LysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly-----Gly 163  
Db 525 ATGACACCAAGATCTTCCATCAACAGCAGGAGCGGGTGCAGATGGGCCAAGCGGC 584  
QY 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*Thr---TyrMetCysValAla 182  
Db 585 AACCTCTACTTTGGCAATGTCTCACCTCCGCAACCACTCAGACTACATCTGC----- 638  
QY 183 ThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln 202  
Db 183 ----- 202

Db 639 -----CACGCCCACTTCCAGGCACACAGGACCATCATTCAGAAG----- 677  
QY 203 AspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeu 222  
Db 678 -----GAACCCATTTGACCTC-----CGGTCAAGGCCACCAAC---AGCATG 716  
QY 223 LeuAenProAspPro-AlaGluGlyProLysProArgProAlaVal-----Tyr-Leu\* 240  
Db 717 ATTGACAGGAAGCGCGCTGCTCTTCCCAACCACTCCAGCAGCCACCTGGTGGCCTTG 776  
QY 240 \*\*TrpLysValSerGlyPro\*\*\*----- 247  
Db 777 CAGGGCAGCCATTTGGTCTGGAGTGCATCCCGAGGCTTTCCACGCCCCACCATCAA 836  
QY 248 -----ArgLeuProAenLeuThrArgProCysSerGlyPro----- 259  
Db 837 TGGCTGGCGCCCGAGTGGCGCCCATCCAGCGCGACCGTGTACCTACCAAGAACCAACAAG 896  
QY 260 -----ArgLeuProArgGluAlaArgG 267  
Db 897 ACCCTGCAGCTGCTGAAAGTGGCGAGGAGGATGATGGCGAGTACCGCTGCTGGCCGAG 956  
QY 267 LuLeuArgGlyGln 271  
Db 957 AACTCACTGGGCGAG 970

RESULT 10  
US-09-041-886-24  
; Sequence 24, Application US/09041886  
; Patent No. 6235872  
; GENERAL INFORMATION:  
; APPLICANT: Bredesen, Dale E.  
; APPLICANT: Rabizadeh, Sharoz  
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/041,886  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2626  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4608 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..4342  
; US-09-041-886-24

Alignment Scores:  
Pred. No.: 6,818-08 Length: 4608



Score: 206.00 Matches: 68  
Percent Similarity: 42.80% Conservatives: 36  
Best Local Similarity: 27.98% Mismatches: 97  
Query Match: 13.97% Indels: 42  
DB: 3 Gaps: 11

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-09-041-886-24 (1-4608)

QY 24 MetSerCysArgAlaSerGlyGlnProProThrThrLeuLeuAsnGlyGln 43  
DB 475 CTCAGTGTGAAGTCAATGGGAGGCCATGCCAACATCCATGCGAGAGAACCAACAA 534

QY 44 ProLeuSerMetValProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 62  
DB 535 GACCTGACTCCCAATCCAGGTGACTCCCGAGTGGTGTCTTGCCTCTGGAGCAATGGCAG 594

QY 63 Leu-----LeuGlnProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
DB 595 ATCAGCCGACTCCACCG-----GGG 615

QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 99  
DB 616 GACATGGAATTTACGATGCTCAGCTCGAAT-----CCAGCCAGCTCAGAACAA 666

QY 100 GlyAlaArgLeuSerValAlaValLeuArgGluAsp-----Phe 112  
DB 667 GAAATGAAGCAGAGTCAAGATTTTATCAGATCCAGGACTGCATAGACAGCTGTATTTT 726

QY 113 GlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 132  
DB 727 CTCGAAAGACCAATCAATGTAGTACCATTTGAAGGAAAAGATGCTGTCTGGAATGTTGT 786

QY 133 ProProTyrGlyHisProGluProThrValSerTyrTyrLysAspGlyLysProLeuAla 152  
DB 787 GTTCTCT---GGTATCTCTCCACAGTTTACTGTGTACGAGGCGAGGAGTCAACAA 843

QY 153 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 171  
DB 844 CTCAGGTCTAAAAGATTTCTTTATTGGTGGTGAAGCAACTTGTCTTCAATGTGACA 903

QY 172 LysSerAspGlu---ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 191  
DB 904 GATGATGACAGTGGGAATGTATACCTGTGTGTGCACATATATAAAATGAGAATATTAGTGCC 963

QY 192 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeu 211  
DB 964 TCTGACAGCTCAGAGTCTGTGTGTCGCGCATGGTTTTTAATCATCTCTTCCAACTGTAT 1023

QY 212 Ala-----ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 228  
DB 1024 GCCTATGAAGCATGGATATTGAGTTGATGTACAGTC-----1062

QY 229 GluGlyProLysProArgProAlaValTyrLeu---TyrLysValSerGlyPro---Arg 248  
DB 1063 ---CTGGAAGCCTGTGCCCACTGTG-----AATTGGATGAAGATGAGATGTGTC 1113

QY 249 LeuProAsn 251  
DB 1114 ATTCCTAGT 1122

## RESULT 11

PCT-US94-05277-1

; Sequence 1, Application PC/TUS9405277

; GENERAL INFORMATION:

; APPLICANT: Bruskin, Arthur

; APPLICANT: Jarosz, David E.

; APPLICANT: Johnson, Karen

; APPLICANT: Kinzler, Kenneth W.

; APPLICANT: Vogelstein, Bert

; APPLICANT: Zaretsky, James R.

; TITLE OF INVENTION: Antibodies Specific for DCC Gene Product

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie & Beckett  
STREET: 1001 G Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05277  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42709  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202.508.9100  
TELEFAX: 202.508.9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4608 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 18q21  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4342  
PCT-US94-05277-1

## Alignment Scores:

Pred. No.: 6.81e-08 Length: 4608  
Score: 206.00 Matches: 68  
Percent Similarity: 42.80% Conservatives: 36  
Best Local Similarity: 27.98% Mismatches: 97  
Query Match: 13.97% Indels: 42  
DB: 5 Gaps: 11

US-10-047-021-86\_COPY\_28\_303 (1-276) x PCT-US94-05277-1 (1-4608)

QY 24 MetSerCysArgAlaSerGlyGlnProProThrThrLeuLeuAsnGlyGln 43  
DB 475 CTCAGTGTGAAGTCAATGGGAGGCCATGCCAACATCCATGCGAGAGAACCAACAA 534

QY 44 ProLeuSerMetValProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 62  
DB 535 GACCTGACTCCCAATCCAGGTGACTCCCGAGTGGTGTCTTGCCTCTGGAGCAATGGCAG 594

QY 63 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
DB 595 ATCAGCCGACTCCACCG-----GGG 615

QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArg--- 99  
DB 616 GACATGGAATTTACGATGCTCAGCTCGAAT-----CCAGCCAGCTCAGAACAA 666

QY 100 GlyAlaArgLeuSerValAlaValLeuArgGluAsp-----Phe 112  
DB 667 GAAATGAAGCAGAGTCAAGATTTTATCAGATCCAGGACTGCATAGACAGCTGTATTTT 726

QY 113 GlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 132  
DB 727 CTCGAAAGACCAATCAATGTAGTACCATTTGAAGGAAAAGATGCTGTCTGGAATGTTGT 786

Db 727 CTGCAAGACCAATCAATGTAGTAGCATTGAAGGAAAGATGCTGCTCGAATGTGT 786  
Qy 133 ProProTrrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAla 152  
Db 787 GTTCTCT---GGCTATCCTCCACCAAGTTTACCTGGTTACGAGCGGAGAGTCAATCAA 843  
Qy 153 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 171  
Db 844 CTCAGGCTAAAGATATCTTTATTTGGTGGAGAGCACTTGCTTATCTCCAATGTGACA 903  
Qy 172 LysSerAspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSer 191  
Db 904 GATGATGACAGTGAATGATATACCTGTCTGTCTCATATAAATAAGATATAGTGC 963  
Qy 192 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeu 211  
Db 964 TCTGAGAGCTCACAGTCTTGGTTCGCCCATGGTTTAAATCATCTCTTCCAACCTGTAT 1023  
Qy 212 Ala-----ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAla 228  
Db 1024 GCCTATGAAGCATGGATATTGATTTGAATGTACAGTC-----1062  
Qy 229 GluGlyProLysProArgProAlaValTrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*Arg 248  
Db 1063 ---TCTGAAAGCCTGTGCCCACTGTG-----AATTGGATGAAGATGGAGATGTGTC 1113  
Qy 249 LeuProAsn 251  
Db 1114 ATTCTAGT 1122

## RESULT 12

US-09-638-649-2  
; Sequence 2, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED  
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1426  
; TYPE: DNA  
; ORGANISM: Bos Taurus  
US-09-638-649-2

## Alignment Scores:

Pred. No.:	5.96e-08	Length:	1426
Score:	199.00	Matches:	89
Percent Similarity:	38.63%	Conservative:	35
Best Local Similarity:	27.73%	Mismatches:	122
Query Match:	13.49%	Indels:	76
DB:	4	Gaps:	17

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-09-638-649-2 (1-1426)

Qy 5 ProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly---ProGlyProAlaArg 23  
Db 376 CCAGAAAT---GTTGATCGCTCTGAATCATAGCTGTGTGCTCCCAATAAGTGGGG 432  
Qy 24 MetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuAsnGlyGln 43  
Db 433 ACATGTGTCCGAGGGGGGTACCTCGAGGGACTCTTAATCTGCTCTTGATGGGAAA 492  
Qy 44 ProLeuSerMetValProProAspProHisIleLeuLeuProAspGlyThrLeuLeu 63  
Db 493 ACT-----CTGATTCTCTGATGGCAAGAGGTGTCA 522

Qy 64 LeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThrAspLeu 82  
Db 523 GTGAGGAGAGACCAAGACACACCCAAAGACAGGGCTTTTCAGCTCCATTCGGAGCTG 582  
Qy 83 GlyVal-----TyrThrCysGluAlaSer---90  
Db 583 ATGCTGACCCAGCTCGGGGAGAGCTCTCACCCACCTTCTCTGTAGCTTCAACCCT 642  
Qy 91 -----AsnArgLeuGlyThrAlaVal-----97  
Db 643 GGCTTCCCGCGCGAGCCCTGCGACACGGCCCCCATCCAGTCCAGGCTCGAGGTCTGAGTGAG 702  
Qy 98 -----SerArgGlyAlaArgLeuSerValAlaValLeuArgGlu---AspPheGln 113  
Db 703 CACCGAGTGGGAGGGCCCAACAGTGGAGCGCTGTGCCACTGAAGAGTCCAGTGGTG 762  
Qy 114 IleGlnProArgAspMetValAlaValIleGlnPheThrLeuGluCysGlyPro 133  
Db 763 GTAGAGCCAGAGGGGAGCAGTAGCTCTCTGGTGTACTGTGACCTTGACCTGTGAAGCC 822  
Qy 134 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 153  
Db 823 CCC---GCCAGAGCCCCACCTCAATCCACTGGATCAAGATGGCAGGCCCTCCCTT 879  
Qy 154 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 173  
Db 880 CCCCT-----GGCCCCATGCTGCTCTCCAGAGGTAGGCGCTGAG 921  
Qy 174 AspGlu\*\*\*ThrTyrMetCysValAlaThrAsn---SerAlaGlyHisArgGluSerArg 192  
Db 922 -GACCGGAACTACAGTTGTGTGGCCACCATCCAGCCATGGGCCCCAGGAGGCGGT 981  
Qy 193 AlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAla 212  
Db 982 GCTGTACGCTCAGATCATCGAA-----ACAGCGAGGAGGGAGACACTGCA 1029  
Qy 213 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 232  
Db 1030 GGCTCTGTGAAGGGCGGGCTGGAAACCTTAGC-CTGACCTTGGGGATCTCGGGAGG 1088  
Qy 233 Pro-----ArgProAlaValTrp-----Leu\*\*\*TrpLysValSer-----244  
Db 1089 CCTGGGAGACAGTCGCTGCTCATTTGGGTGTCGTGTGGATCGAAGGGCGCAACGCAA 1148  
Qy 245 -----GlyPro\*\*\*ArgLeu-----ProAsnLeuThr 253  
Db 1149 AGCAGAGGAGGAAGGTCCCGGAAACACAGGAGGAGAGAGAGGAGAGCGGAAT 1208  
Qy 254 ArgProCysSerGlyProArgLeuProArgGlu-----AlaArgGluLeuArgGlyGln 271  
Db 1209 GAACCAAG 1268  
Qy 272 Arg 272  
Db 1269 CGG 1271

## RESULT 13

US-08-427-497E-6  
; Sequence 6, Application US/08427497E  
; Patent No. 5969124  
; GENERAL INFORMATION:  
; APPLICANT: Lemmon, Vance  
; TITLE OF INVENTION: A Method for Characterizing the  
; TITLE OF INVENTION: Nucleotide Sequence of LicAM and  
; Patent No. 5969124  
; TITLE OF INVENTION: the Nucleotide Sequence  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
; ADDRESSEE: Minnich & McKee  
; STREET: 1100 Superior Avenue

STREET: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
MEDIUM TYPE: Storable  
COMPUTER: Compaq Prolinea 5100e  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/427,497E  
FILING DATE: April 24, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/904,991  
FILING DATE: June 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
TELEX: (216) 980162  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1042  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: nucleic acids  
HYPOTHETICAL: irrelevant  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: homo sapiens  
INDIVIDUAL ISOLATE: 17-18 week fetus  
IMMEDIATE SOURCE:  
LIBRARY: Stratagene CDNA Library 936206  
CLONE: C2  
PUBLICATION INFORMATION:  
AUTHORS: Hlavin, Mary Louise  
TITLE: Molecular structure and functional testing of human L1CAM: an interspecies comparison.  
JOURNAL: GENOMICS  
VOLUME: 11  
ISSUE:  
PAGES: 416-423  
DATE: 1991  
RELEVANT RESIDUES IN SEQ ID NO: -26 to 1016  
US-08-427-497E-6

Alignment Scores:  
Pred. No.: 4,86e-08 Length: 1042  
Score: 198.00 Matches: 88  
Percent Similarity: 36.59% Conservative: 32  
Best Local Similarity: 26.83% Mismatches: 106  
Query Match: 13.42% Indels: 102  
DB: 2 Gaps: 19

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-08-427-497E-6 (1-1042)

QY 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
::: ||||| ::::::::::||| ||| :::  
141 GAACAGTCTCCAGCGCGCTGTGTCTTCCCAAGATGACATC----- 185

QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProThrIleArgTrpLeuLeu 40  
::: ||||| ::::::::::||| ||| |||||  
186 -----AGCTTCAAGTGTGAGCGCCAGTGGCAAGCGGAGTGCATGCTCGGTGACGAGG 239

QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60

ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
MEDIUM TYPE: storable  
COMPUTER: Compaq Prolinea 5100e  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/341-843B  
FILING DATE: No. 5872225ember 18, 1994  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/904,991

FILING DATE: June 26, 1992

## ATTORNEY/AGENT INFORMATION:

NAME: Minnich, Richard J.

REGISTRATION NUMBER: 24,175

REFERENCE/DOCKET NUMBER: CWR 2 149-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (216) 861-5582

TELEFAX: (216) 241-1666

TELEX: (216) 980162

## INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 3774

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: irrelevant

ANTI-SENSE: no

## ORIGINAL SOURCE:

ORGANISM: Homo Sapiens

INDIVIDUAL ISOLATE: 17-18 week fetus

## IMMEDIATE SOURCE:

LIBRARY: Stratagene cDNA Library 936206

CLONE: synthesis of 4 clones

## PUBLICATION INFORMATION:

AUTHORS: Hlavin, Mary Louise

AUTHORS: Lemmon, Vance

TITLE: Molecular structure and functional

TITLE: testing of human L1CAM: an

TITLE: interspecies comparison.

JOURNAL: GENOMICS

VOLUME: 11

ISSUE: 11

PAGES: 416-423

DATE: 1991

RELEVANT RESIDUES IN SEQ ID NO: 1 to 3774

## US-08-341-843B-1

## Alignment Scores:

Pred. No.:	2,47e-07	Length:	3774
Score:	198.00	Matches:	88
Percent Similarity:	36.59%	Conservative:	32
Best Local Similarity:	26.83%	Mismatches:	106
Query Match:	13.42%	Indels:	102
DB:	2	Gaps:	19

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-08-341-843B-1 (1-3774)

Qy	1	GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly	20
Db	115	GAACAGCTCCACGGCGCTGGTGTCTTCCACAGATGATC	159
Qy	21	ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu	40
		---	---

Db	160	-----AGCCTCAAGTGTGAGCCAGTGGCAAGCCCGAAGTGCAGTTCCGCTGACGAGG	213
Qy	41	AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr	60
Db	214	GATGGTGTCTC-----CACTTCAACCCAGGAAGAG	243
Qy	61	Leu-----LeuLeuLeuGlnProProAlaAargGlyHisAlaHisAspGlyGlnAlaLeu	78
Db	244	CTGGGTGTGACCGTGTACCACTGCGCC-----CACTCTGGCTCTCTCCACC	288
Qy	79	SerThrAsp-----LeuGlyValTyrThrCysGluAla	89
Db	289	ATCAGGGGCAACACACAACTTTGTCTCAGAGGTTCAGGGCATCTACCGCTGTTTGGCC	348
Qy	90	SerAsnArgLeuGlyThrAlaValSerArgGlyAlaAargLeuSerValAlaValLeuArg	109
Db	349	AGCAATAAGCTGGGACCCGATGTCATGATCCATGAGATCCGGCTC-----ATGGCC	396
Qy	110	GluAspPheGlnIleGlnProArgAspMetValAlaVal-----GlyGlu	125
Db	397	GAGGTGCCCCCAAGTGGCCAAAGGAGACAGTGAAGCCCGTGGAGGTGGAGAGGGGAG	456
Qy	126	GlnPheThrLeuGlyCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp	145
Db	457	TCAGTGGTCTCTGCTTGCACACCTCC-----CCAAGTGCAGAGCCTCTCCGATCTACTGG	513
Qy	146	LysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly-----Gly	163
Db	514	ATGAACAGCAAGATCTTGACATCAGCAGCAGCGGGTGCAGTGGGCCAGAACCGC	573
Qy	164	SerLeuLeuMetAlaArgAlaGluLysSerAspGlu***Thr---TyrMetCysValAla	182
Db	574	AACCTCTACTTGGCAATGTGCTCACCTCCGACAAACCACTCAGACTACATCTGC-----	627
Qy	183	ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln	202
Db	628	-----CACGCCCACTTCCAGGCACCAAGACCATCATTCAGAA-----	666
Qy	203	AspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeu	222
Db	667	-----GAACCAATTGACCTC-----CGGTCAAGGCCCAACAC-----AGCATG	705
Qy	223	LeuAsnProAspProAlaGluGlyProLysProArgProAlaVal-----	237
Db	706	ATTGACAGGAAGCGCGCTGCTTCCCCCACTCCAGCAGCCACCTGGTGGCTTG	765
Qy	238	-----TrpLeu***TrpLysValSerGlyPro***ArgLeuPro-----	250
Db	766	CAGGGGCAGCATTGG---TCCTGGAGTGCATCG---CCGAGGGCTTTCCACGCCCAACC	819
Qy	251	-----AsnLe	252
Db	820	ATCAATGGCTGCGCCCAAGTGGCCCATGCCAGTGCACCTGTCACCTACCAGAACAC	879
Qy	252	uThrArgProCysSer-GlyPro-----ArgLeuProArgGluA	265
Db	880	AACAAGACCTGCAGCTGTGAAAGTGGCGGAGGAGGATGATGGCGATCCGCTGCTG	939
Qy	265	laArgGluLeuArgGlyGln	271
Db	940	GCCGAGAACTCACTGGGCAG	959

## RESULT 15

US-08-427-497E-1

Sequence 1, Application US/08427497E

Patent No. 5969124

GENERAL INFORMATION:

APPLICANT: Lemmon, Vance

TITLE OF INVENTION: A Method for Characterizing the

TITLE OF INVENTION: Nucleotide Sequence of L1CAM and

Patent No. 5969124

TITLE OF INVENTION: the Nucleotide Sequence

TITLE OF INVENTION: Characterized Thereby

NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Pagan,  
ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
STREET: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
MEDIUM TYPE: storable  
COMPUTER: Compaq Prolinea 5100e  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/427,497E  
FILING DATE: April 24, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/904,991  
FILING DATE: June 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
TELEX: (216) 980162  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3774  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: nucleic acids  
HYPOTHETICAL: irrelevant  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
INDIVIDUAL ISOLATE: 17-18 week fetus  
IMMEDIATE SOURCE:  
LIBRARY: Stratagene cDNA Library 936206  
CLONE: synthesis of 4 clones  
PUBLICATION INFORMATION:  
AUTHORS: Hlavin, Mary Louise  
AUTHORS: Lemmon, Vance  
TITLE: Molecular structure and functional  
TITLE: testing of human LiCAM: an  
TITLE: interspecies comparison.  
JOURNAL: GENOMICS  
VOLUME: 11  
ISSUE:  
PAGES: 416-423  
DATE: 1991  
RELEVANT RESIDUES IN SEQ ID NO: 1 to 3774  
US-08-427-497E-1

Alignment Scores:  
Pred. No.: 2,47e-07 Length: 3774  
Score: 198.00 Matches: 88  
Percent Similarity: 36.59% Conservative: 32  
Best Local Similarity: 26.83% Mismatches: 106  
Query Match: 13.42% Indels: 102  
DB: 2 Gaps: 19

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-08-427-497E-1 (1-3774)

Qy 1 GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20  
Db 115 GAACAGTCTCCAGCGCGCTGGTTGTCTTCCCAACAGATGACATC----- 159

Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTyrLeuLeu 40  
Db 160 -----AGCCTCAAGTGTGAGCCAGTGGCAAGCCGGAAGTTCGCTCGGACGAGG 213  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db 214 GATGGTGTC-----CACTTCAAAACCAAGGAAGAG 243  
Qy 61 Leu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeu 78  
Db 244 CTGGGTGTGACCGGTGTACCACTCGCC-----CACTCTGGGTCTCTTACC 288  
Qy 79 SerThrAsp-----LeuGlyValTyrCysGluAla 89  
Db 289 ATCAGGGCAACAACAGCAACTTTGCTCAGAGGTTCCAGGGCATCTACCGCTGCTTTGCC 348  
Qy 90 SerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArg 109  
Db 349 AGCAATAGCTGGGCAACCGCCATGTCCCATGAGATCCGGCTC-----ATGGCC 396  
Qy 110 GluAspPheGlnIleGlnProArgAspMetValAlaVal-----GlyGlu 125  
Db 397 GAGGTGCCCCCAAGTGGCCAAAGAGACAGACAGTGAAGCCCGTGGAGTGGAGGAAGGGAG 456  
Qy 126 GlnPheThrLeuGluCysGlyProProTyrGlyHisProGluProThrValSerTyrTrp 145  
Db 457 TCAGTGGTTCCTGCTTGGCAACCTCCC-----CCAAGTGCAGAGCCTCTCCGGATCTACTGG 513  
Qy 146 LysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly-----Gly 163  
Db 514 ATGAACAGCAAGATCTTGCACATCAAGCAGCAGCAGCGGTGACGATGGCGCAGACGCG 573  
Qy 164 SerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*Thr---TyrMetCysValAla 182  
Db 574 AACCTTACTTTGCCAATGTGCTCACTCCGACAACTCAGACTACTATCTGC----- 627  
Qy 183 ThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGln 202  
Db 628 -----CAGGCCCACTTCCAGGCACCGAGGACCATCTTCAAG----- 666  
Qy 203 AspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnValThrLeu 222  
Db 667 -----GAACCCATTGACCTC-----CGGTCAAGGCCCAAC-----AGCATG 705  
Qy 223 LeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal----- 237  
Db 706 ATTGACAGGAAGCGCGCTGCTCTTCCCACTCCAGCAGCCACTCGTGGCCCTTG 765  
Qy 238 -----TrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*ArgLeuPro----- 250  
Db 766 CAGGGGCAGCCATTGG---TCCTGGAGTGCATCG---CCGAGGGCTTTCCCAACGCCACC 819  
Qy 251 -----AsnLe 252  
Db 820 ATCAAAATGGCTGCGCCCGCAGTGGCCCATGCCAGTGCACCTGCTACCTACCAGAACCCAC 879  
Qy 252 uThrArgProCysSer-GlyPro-----ArgLeuProArgGluA 265  
Db 880 AACCAAGACCTTCAGCTGCTGAAAGTGGCGAGGAGATGATGGCGGATGACCGTGCCTG 939  
Qy 265 LaArgGluLeuArgGlyGln 271  
Db 940 GCCGAGAACTCACTGGGCGAG 959

Search completed: January 31, 2004, 15:30:59  
Job time : 74.5389 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: January 31, 2004, 14:37:41 ; Search time 303.648 Seconds  
(without alignments)  
3312.713 Million cell updates

**Title:** US-10-047-021-86 COPY 28 303

**Perfect score:**

Sequence: 1 QDSPPQILVHPQDLFQPG.....SGPRLPREARELRGQRRNTG 276

Scoring table: BLOSUM62

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Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0

Maximum DB seq length: 2000000000  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

100% Processing. Maximum Match 100%

Listing first 45 summaries

**Command line parameters:**

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-Q/cgn2/USPTO.spool_p/US10047021/runat_30012004.145455.24678/app_query.fasta.1.910
-DB=Published Applications NA -QMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOCUS=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DLOCAL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10047021.c@CgN2.1.129.0runat_30012004.145455.24678
-NCPU=6 -ICPU=3 -NO MMAP -LARGEXQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LOGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :	Published Applications	NA:*
1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*	
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*	
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*	
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*	
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*	
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*	
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*	
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9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*	
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*	
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18:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

## ALIGNMENTS

## RESULT 1

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US-10-047-021-31
; Sequence 31, Application US/10047021
; Publication No. US20040002591A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ0162
; CURRENT APPLICATION NUMBER: US/10/047,021
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/262,066
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: PCT/US98/18360
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: US 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,669
; PRIOR FILING DATE: 1997-09-05

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; PRIOR APPLICATION NUMBER: US 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (637)..(637)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (850)..(850)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-047-021-31
Alignment Scores:
Pred. No.: 2,59e-131 Length: 1346
Score: 1469.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.59% Indels: 0
DB: 12 Gaps: 0
US-10-047-021-86_COPY_28_303 (1-276) x US-10-047-021-31 (1-1346)
Qy 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 112 CAGGACTCCCGCCCGCCAGATCTTAGTCCACCCCGAGGACAGCTGTTCCAGGGCCCTGGC 171
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArgTrpLeuLeu 40
Db 172 CCTGCAGGATGAGCTGCGAGCCTCAGGCGAGCCACCTCCACCATCCGCTGGTGTGTG 231
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 232 AATGGCAGCCCTGAGCATGTGTCGCCCGGAGCATGCCACACACCTCTCCCTGATGGGACC 291
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 292 CTCTGCTGTACAGCCCTGCGCGGGAGCATGCCACGATGGCCAGGCCCTGTCCACA 351
Qy 81 AspLeuGlyValThrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 352 GACCTGGGTGTCTACATATGAGGCCAGCAACCGCTTGGCAGCGAGTCAGCAGAGGC 411
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 412 GCTCGGTGTCTGTGGCTGTCTCTCGGAGGATTTCCAGATCCAGCCCTCGGGACATGGTG 471
Qy 121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 472 GCTGTGGTGGTGAGCAGTTTACTCTGAATGTGGCGCCCTCCAGGCCACCCAGAGCCC 531
Qy 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 532 ACAGTCTCATGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGGAAGCACACAGTG 591
Qy 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTrpMetCys 180
Db 592 TCCGGGGGGTCCCTCTGATGCAAGACAGAGAGAGTGCAGGAAGACCTACATGTGT 651
Qy 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
Db 181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
652 GTGGCCACCAACAGCGCAGGACACAGGGAGAGCGCGCAGCGCGGTTTCCATCCAGGAG 711
Qy 201 ProGlnAspTyThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 220
Db 712 CCCAGGACTACAGCGAGCCTGTGGAGCTTCTGGCTGTGGCAATTACGCTGGAAATGTG 771
Qy 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
Db 772 ACATCTCTGAACCGGATCTCTGCAGARGGCCCAAGCCTAGACCGGGGTGTGGCTCARG 831
Qy 241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProArg 260
Db 832 TGAARGTCACTGGCCCTTNTGCGCTTGTACAGCGCTTGTTCAGGAGCCACAGA 891
Qy 261 LeuProArgGluAlaArgGluLeuArgGlyGlnArgArgAsnThrGly 276
Db 892 CTGCCCCGGGAGGCCAGGGAGCTCCGTGGCGCAGAGGAGGAGAACACAGGA 939
RESULT 2
US-10-411-224-31
; Sequence 31, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
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; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
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US-10-047-021-86_COPY_28_303 (1-276) x US-10-411-224-31 (1-1346)
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Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProProThriIleArgTriLeuLeu 40  
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Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
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Qy 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
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Db TGGAAAGTCACTGGCCCTTTGCGCTGCCCCATCTTACACGGCCCTTGTTCAGGACCCAGA 891  
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US-03-978-295A-210  
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; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
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Db 253 CTTCTGTGCTACAGCCCCCTGCCGGGAGCATGCCACCATGCGCCAGGCGCTGTCCACA 312
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; GENERAL INFORMATION:  
; APPLICANT: Aekhenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 2,72e-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservatives: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 10 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-697-210 (1-3716)

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Db 253 CTTCTGCTGTACAGCCCTGCGCGGGGACATGCCACCATGGCCAGGCGCTGTCCACA 312
Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Length: 3716  
Matches: 268  
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Mismatch: 3

Query Match: 97.08% Indels: 1  
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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen



APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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Alignment Scores:
Pred. No.: 2,72e-127 Length: 3716
Score: 1432.00 Matches: 268
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Query Match: 97.08% Indels: 1
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US-10-047-021-86_COPY_28_303 (1-276) x US-09-999-832A-210 (1-3716)

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Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeu 40
Db 133 CTGTCAGGATGAGCTGCGCAGCTCAGGACCACTCCACCATCCGCTGGTGTG 192
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGCAGCCCTGAGCATGTGCGCCCGCAGACCCACACCACTCTGCTGTATGGGACC 252
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 253 CTTCGTGCTACAGCCCCCTGCGCGGGAGATGCCACGATGGCCAGGCCCTGTCCACA 312
Qy 81 AspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100

313 GACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGCCACGGCAGTCAGCAGAGGC 372
101 AlaArgLeuSerValAlaValLeuAraGluAspPheGlnIleGlnProArgAspMetVal 120
373 GCTCGGCTGTCTGGGTGCTCTCCCGGAGAGATTCCAGATCCAGCCTCGGGAGCATGGTG 432
121 AlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
433 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCGCCCTGGGGCCACCCAGAGCCC 492
141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
493 ACAGTCTCATGTGGAAAGATGGAAACCCCTGCGCCCTCCAGCCCGGAAGGCACACAGTG 552
161 SerGlyGlySerLeuLeuMetAlaAraGluLysSerAspGlu***ThrTyMetCys 180
553 TCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTGCAGAGGACCTCATGTGT 612
181 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 200
613 GTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCGCGGCTTCCATCCAGGAG 672
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733 ACATGCTGAACCGCGATCTTGAGAGGGGCCCAAGCCTAGACCGCGGCTGTGGCTCAGC 792
241 TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260
793 TGGAGGTGAGTGGCCCTGCTGGCCCTGCCCTTACACGGGCTTGTTCAGGACCCAG 852
260 gLeuProArgGluAlaArgGluLeuArgGlyGlnArg 272
853 ACTGCCCGGGAGCGCAGGAGCTCGTGGGCAGAG 899

RESULT 7
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; Sequence 210, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
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2 CURRENT FILING DATE: 2001-10-15  
3 PRIOR APPLICATION NUMBER: 09/918585  
4 PRIOR FILING DATE: 2001-07-30  
5 PRIOR APPLICATION NUMBER: 60/062250  
6 PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
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Percent Similarity: 98.53% Conservative: 1  
Best Local Similarity: 98.17% Mismatches: 3  
Query Match: 97.08% Indels: 1  
DB: 11 Gaps: 0

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Db 133 CTGCGCAGGTAGCTGCGAGCTCAGGCTCAGGCGAGCCATCTCCACCATCCGCTGGTGTG 192  
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Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
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Qy 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
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Qy 201 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 220

Db 673 CCCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGCGAATTCAGCTGGAATGTG 732  
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Db 733 ACAGTGTGAACCCGGATCTCTGAGAGGGCCCAAGCCTAGACCGGGGTGTGGCTCAGC 792  
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Db 793 TGAAGGTAGTGGCCCTGCTGGCCCTGCCAATCTTACACGGCTTGTTCAGGACCAG 852  
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Db 853 ACTGCCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 889

## RESULT 8

US-09-978-608A-210  
; Sequence 210, Application US/09978608A  
; Publication No. US20030045462A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C22  
; CURRENT APPLICATION NUMBER: US/09/978,608A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 210  
; LENGTH: 3716  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-978-608A-210

Alignment Scores:  
Pred. No.: 2,72e-127 Length: 3716  
Score: 1432.00 Matches: 268  
Percent Similarity: 98.53% Conservative: 1  
Best Local Similarity: 98.17% Mismatches: 3  
Query Match: 97.08% Indels: 1  
DB: 11 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-09-978-608A-210 (1-3716)

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QY 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
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Db 193 AATGGCAGCCCTGAGCATGTGGCCCGCAGACCCACACCATCTCTGCTGATGGGACC 252
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 253 CTTCTGCTGTACAGCCCTTCCCGGGACATGCCCCAGATGGCCAGCCCTGTCCACA 312
QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTGTCTACATGTGAGCGCCAGCAACCGGCTTGGCAGCGCATGCAGAGGC 372
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgMetVal 120
Db 373 GCTCGGCTGTCTGCTGCTCTCCGGGAGGATTTCCAGATCCAGCTCGGGACATGGTG 432
QY 121 AlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 433 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCCGCCCTGGGGCCACCCAGAGCC 492
QY 141 ThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrVal 160
Db 493 ACAGTCTCATGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAGGCACACAGTG 552
QY 161 SerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***ThrTyrMetCys 180
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Db 613 GTGGCCACCCAGCCGAGCATAGGGAGAGCCCGCAGCCCGGGTTCATCCAGGAG 672
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QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTrpLeu*** 240
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Db 793 TGGAAAGGTGAGTGGCCCTGCTGCGCTGCCCCAATCTTACACGGCCCTTGTTCAGGACCCAG 852
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; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
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; SEQ ID NO 210
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; ORGANISM: Homo sapiens
US-09-978-585A-210

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Pred. No.: 2,72e-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservatives: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 11 Gaps: 0

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QY 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
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; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
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; GENERAL INFORMATION:



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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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1	APPLICANT: Stewart, Timothy A.	60/078004
2	APPLICANT: Tumas, Daniel	60/078004
3	APPLICANT: Williams, P. Mickey	60/078004
4	APPLICANT: Wood, William I.	60/078004
5	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	60/078004
6	TITLE OF INVENTION: Acids Encoding the Same	60/078004
7	FILE REFERENCE: P2630PIC25	60/078004
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9	CURRENT FILING DATE: 2001-10-16	60/078004
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/ PRIOR APPLICATION NUMBER: 60/085573  
/ PRIOR FILING DATE: 1998-05-15  
/ PRIOR APPLICATION NUMBER: 60/085704  
/ PRIOR FILING DATE: 1998-05-15  
/ PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2,728-127 Length: 3716  
Score: 1432.00 Matches: 268  
Percent Similarity: 98.53% Conservativity: 1  
Best Local Similarity: 98.17% Mismatches: 3  
Query Match: 97.08% Indels: 1  
DB: 11 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-09-978-564A-210 (1-3716)

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Db 133 CTGCCAGATGAGTGCACAGCCTCAGGCCAGCCACCTCCACCATCCGCTGGTGTG 192  
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db 193 AATGGCAGCCCTGAGCATGTGCCCCCAGACCACACACCTCTGCTGCTGATGGACC 252  
Qy 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db 253 CTTCCTGCTCAGCCCTCCCGGGGACATGCCACGATGGCCAGCCCTGTGCCACA 312  
Qy 81 AspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db 313 GACCTGGGTGTACACATGTAGGCCACCAACCGGCTTGGCAGCGCAGTCCAGAGGC 372  
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db 373 GCTCGGCTGCTGTGGCTGCTCCGGGAGGATTTCCAGATCCAGCTCGGGACATGGTG 432  
Qy 121 AlaValValGlyGlnPheThrLeuGlyCysGlyProProTrpGlyHisProGluPro 140  
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Db 553 TCCGGGGGGTCCCTGCTGATGCGCAAGAGCAGAGAGAGTGTGACGAAGGACCTACATGTGT 612  
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Db 853 ACTGCCCGGAGGCGCAGGAGCTCCGTGGGCGAGAGG 889

## RESULT 13

US-09-999-833A-210  
; Sequence 210, Application US/09999833A  
; Publication No. US20030054405A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrata, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C65  
; CURRENT APPLICATION NUMBER: US/09/999,833A  
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; PRIOR APPLICATION NUMBER: 09/918585  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2, 72e-127 Length: 3716  
Score: 1432.00 Matches: 268  
Percent Similarity: 98.53% Conservative: 1  
Best Local Similarity: 98.17% Mismatches: 3  
Query Match: 97.08% Indels: 1  
DB: 11 Gaps: 0

US-10-047-021-86\_COPY\_28\_303 (1-276) x US-09-999-833A-210 (1-3716)

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QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
DB 193 AATGGCAGCCCTCAGCATGTGTGCCCCAGACCCACACCCACCTCTCGCTGATGGGACC 252
QY 61 LeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
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RESULT 14

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; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
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; APPLICANT: Gao, Wei-Qiang  
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; APPLICANT: Tumas, Daniel  
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; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630F1C12  
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; CURRENT FILING DATE: 2001-10-16  
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Alignment Scores:

Pred. No.:	2.72e-127	Length:	3716
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Percent Similarity:	98.53%	Conservative:	1
Best Local Similarity:	98.17%	Mismatches:	3
Query Match:	97.08%	Indels:	1
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US-10-047-021-86\_COPY\_28\_303 (1-276) x US-09-981-915A-210 (1-3716)

Qy	1	GlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGlyProGly	20
Db	73	CAGGACTCCCGCCCGCCAGATCTTAGTCCACCCAGACCCAGCTGTTCCAGGCGCCCTGC	132
Qy	21	ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTyrIleuLeu	40
Db	133	CCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCAGCCACTCCCATCGCTGTTGCTG	192



QY 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60  
Db 193 AATGGGAGCCCTGAGCATGTGCCCCAGACCCACACCACTCTCTGCTGATGGACC 252  
QY 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80  
Db 253 CTTCTGCTGCTACAGCCCTCTCCCGGGGACATGCCCAGATGGCGCCCTGTCCACA 312  
QY 81 AspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100  
Db 313 GACCTGGGTGTCTACATGTGAGCGCCAGCAACCGCTTGGCAGCGCAGTACAGAGCC 372  
QY 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120  
Db 373 GCTGGCTGTCTGTGGTGTCTCTCGGGAGGATTTCCAGATCCAGCCCTCGGGACATGTG 432  
QY 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTyrGlyHisProGluPro 140  
Db 433 GCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGCGCCCTTGGGGCCACCCAGAGCC 492  
QY 141 ThrValSerTyrTyrLeuAspGlyLysProLeuAlaLeuGlnProGlyValHisThrVal 160  
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Db 553 TCCGGGGGTCTCTGCTGATGSCAAGACAGAGAGATGAGAGGAGCCCTACATGTGT 612  
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QY 221 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaValTyrLeu\*\*\* 240  
Db 733 ACATCTGTGACCCGGATCTGACAGAGGCCCCAGAGCTAGACCCGGGTGTGGCTCAGC 792  
QY 241 TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260  
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QY 260 GlnProArgGluAlaArgGluLeuArgGlyGlnArg 272  
Db 853 ACTGCCCGGGAGCGCAGGAGCTCCGTGGGCGAGAG 889

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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Acids Encoding the Same  
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 2,72e-127 Length: 3716
Score: 1432.00 Matches: 268
Percent Similarity: 98.53% Conservative: 1
Best Local Similarity: 98.17% Mismatches: 3
Query Match: 97.08% Indels: 1
DB: 11 Gaps: 0

US-10-047-021-86_COPY_28_303 (1-276) x US-09-978-824-210 (1-3716)

Qy 1 GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGlnGlyProGly 20
Db 73 CAGACTCCCGCCCGCCAGATCTTAGTCCACCCAGAGCCAGCTGTTCAGGGCCCTTGGC 132
Qy 21 ProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrpLeuLeu 40
Db 133 CTTGCCAGGATGAGTGCCTCAAGCCCTCAGGCCAGCCACCTCCACCATCGCTGTTGCTG 192
Qy 41 AsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAspGlyThr 60
Db 193 AATGGGCAGCCCTGAGCATGGTGCCTCCAGAGCCACACACCATCTCTGCTGATGGGACC 252
Qy 61 LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 80
Db 253 CTTCTGCTGTACAGCCCCCTGCCGGGACATGCCCATGAGCCAGGCTTCCTGCACCA 312
Qy 81 AspLeuGlyValTrpThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGly 100
Db 313 GACCTGGGTGCTTACACATGTAGGCCAGCAGCAACCGGCTTGGCAGCGGAGTCAGCAGAGGC 372
Qy 101 AlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProArgAspMetVal 120
Db 373 GCTCGGCTGTCTGTGGTGTCTCCCGGGAGGATTTCCAGATCCAGCCCTCGGGAATGGTG 432
Qy 121 AlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluPro 140
Db 433 GCTGTGGTGGTGAGCAGTTTACTCTGGAATGTGGCCCGCCCTGGGGCCACCCAGAGCCC 492
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QY 241 TrpLysValSerGlyPro\*\*\*-ArgLeuProAsnLeuThrArgProCysSerGlyProAr 260  
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Db 853 ACTGCCCCGGAGGCCAGGGAGCTCCGTGGGCAGAGG 889

Search completed: January 31, 2004, 17:18:27  
Job time : 314.648 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 30, 2004, 15:52:09 ; Search time 13.3472 Seconds  
(without alignments)  
1988.631 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303  
Perfect score: 1475  
Sequence: 1 QDSPQILVHPQDLFGPG.....SGPRLPREARELGRQRTNG 276

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448.5	30.4	1651	T14160	transmembrane rece
2	445.5	30.2	1612	T30805	duttl protein - mo
3	414.5	28.1	1344	T14316	rig-1 protein - mo
4	354.5	24.0	423	T29549	hypothetical prote
5	354.5	24.0	1273	T42405	sax-3 protein - Ca
6	253	17.2	1535	S46224	peroxidase - frui
7	251	17.0	1272	S26180	neurofascin - chic
8	245	16.6	1427	I51669	tumor suppressor -
9	234.5	15.9	1898	S46216	leukocyte antigen-
10	232.5	15.8	1897	T1DHUK	leukocyte antigen-
11	230.5	15.6	1040	A34695	axonal glycoprotei
12	228	15.5	1040	A49156	transient axonal g
13	228	15.5	5175	T20992	hypothetical prote
14	228	15.5	5198	T43290	hemocentin precurs
15	225	15.3	3707	S18252	heparan sulfate pr
16	222	15.1	1912	A56178	protein-tyrosine-p
17	222	15.1	2029	TDFPLK	protein-tyrosine-p
18	220.5	14.9	1894	C54689	protein-tyrosine-p
19	219.5	14.9	1028	A53449	plasmacytoma-assoc
20	219	14.8	1028	I58164	BIG-1 protein - ra
21	218.5	14.8	1501	I58148	protein-tyrosine-p
22	218.5	14.8	1863	S46217	protein-tyrosine-p
23	218.5	14.8	1907	S50893	protein-tyrosine-p
24	215.5	14.6	1443	I50600	neogenin - chicken
25	213.5	14.5	1036	S22383	axinin 1 precursor
26	212.5	14.4	1070	JC4593	protein-tyrosine k
27	209	14.2	267	A38442	probable tumor sup
28	208.5	14.1	1262	B48758	protein-tyrosine-p
29	208.5	14.1	1496	A48758	protein-tyrosine-p

30	208	14.1	1239	1	A32579	neuroglian - fruit
31	206	14.0	1447	2	A54100	tumor suppressor p
32	205	13.9	1328	2	T23007	hypothetical prote
33	204.5	13.9	1499	2	I50212	protein-tyrosine-p
34	203.5	13.8	4391	2	A38096	perlecan precursor
35	201	13.6	1277	2	T30532	neural cell adhesi
36	195.5	13.3	1880	2	T18531	tractin - medicina
37	195.5	13.3	6642	2	T29757	protein UNC-89 - C
38	195	13.2	7962	2	I38346	elastic titin - hu
39	194.5	13.2	1259	2	A43425	Bravo/Nr-CAM cell
40	194.5	13.2	1268	1	A39640	neural cell adhesi
41	192	13.0	1091	2	A58532	glial cell membran
42	191.5	13.0	1091	1	IUCHNL	neural cell adhesi
43	191	12.9	1260	1	S05479	neural cell adhesi
44	191	12.9	1375	2	T13822	frazzled gene prot
45	189	12.8	946	1	A47299	ror-related recept

ALIGNMENTS

RESULT 1

T14160

transmembrane receptor protein Robol - rat  
C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T14160

R:Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.S.;  
Cell 92, 205-215, 1998

A:Title: Roundabout controls axon crossing of the CNS midline and defines a novel subfam

A:Reference number: 217897; MUID:98117249; PMID:9458045

A:Accession: T14160

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1651 <KID>

A:Cross-references: EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:AAC39960.1

C:Function:

A:Description: appears to function as the gatekeeper controlling midline crossing

C:Keywords: transmembrane protein

Query Match 30.4%; Score 448.5; DB 2; Length 1651;

Best Local Similarity 42.2%; Pred. No. 1.9e-26;

Matches 92; Conservative 31; Mismatches 86; Indels 9; Gaps 2;

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Qy	58	DGTLILLQPPARGHAHDQALSTDLGVVTCASNRLGTAVSRGARLSVAVLRDFOIQPR	117
Db	124	SGSLFFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVALLRDDFRQNP	177
Qy	118	DMVAVGQFTLECGPPWGHPEPTVSWWKKPKALQGRHTVSGGSLLMARAEKSDXT	177
Db	178	DMVAVGEPVAVMECPGRGHEPTISWKKGSPLDKDERTIRGKLMITVTRKSDAGK	237
Qy	178	YMCVATNSAGHSRAARVSIQEPQDYTEPVELLAVRI	215
Db	238	YVCVGTNMVGRSKVADVTVLERPSFVKRPSNLAVTV	275

RESULT 2

T30805

duttl protein - mouse

N:Alternate names: Transmembrane receptor protein Robol homolog

C:Species: Mus musculus (house mouse)

C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999

C:Accession: T30805

R:Wu, M.C.; Lowe, N.; Fordham, R.; Rabbitts, P.

submitted to the EMBL Data Library, July 1998

A:Description: The mouse homologue of human DUTTL/H-robol gene: protein sequence and chr

A:Reference number: 220879

A:Accession: T30805

A;Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1612 <YU>

A;Cross-references: EMBL:Y17793; NID:el329712; PID:el329713; PIDN:CAA76950.1

A;Experimental source: brain

C:Genetics:

A:Gene: dutt1

A:Map position: 16

Query Match 30.2%; Score 445.5; DB 2; Length 1612;

Best Local Similarity 41.7%; Pred. No. 3.2e-26;

Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 1 QDSPPQILVHPDQQLFQCGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHH---LLP 57

Db 25 EDFPRIVVHSDDLVSIGEPATLNCKAEGRTPTIWKGERVETDKDPRSHRMLLP 84

Qy 58 DGTLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFQIQPR 117

Db 85 SGLPFLR-----IVHGRKSRPDGVIICVARNVILGEAVSHNASLEVAIILRDDFRQNP 138

Qy 118 DMVAVVGQFTLECGPPHGPPTVSWWKDGKPLAQGRHTVSGSLLMARAKSDXT 177

Db 139 DVMVAVGEPVAMECQPPRGHPPTISWKKDGSPDLDDKDERITIRGGKLMITYTRKSDAG 198

Qy 178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215

Db 199 YVCVTNVMGERSEVAELTVLERPSFKRPSNLAVTV 236

#### RESULT 3

T14316

zig-1 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T14316

R;Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, E.Y.H.P.

submitted to the EMBL Data Library, April 1998

A:Reference number: Z17975

A:Accession: T14316

A;Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1344 <YUA>

A;Cross-references: EMBL:AF060570; NID:g4206385; PID:g4206386; PIDN:AAD11628.1

Query Match 28.1%; Score 414.5; DB 2; Length 1344;

Best Local Similarity 39.9%; Pred. No. 6.4e-24;

Matches 101; Conservative 27; Mismatches 94; Indels 31; Gaps 8;

Qy 1 QDSPPQILVHPDQQLFQCGPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDP--HH-LLP 57

Db 38 EDAMPRIVEQPDLLVVSIGEPATLPCRAEGPRPNIEWKNGARVATAREDPRAHRLLLP 97

Qy 58 DGTLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFQIQPR 117

Db 98 SGALFF---PRIVH---GRRSRPDGVIICVARNVILGEAAASNASLEVAIILRDDFRQSPG 151

Qy 118 DMVAVVGQFTLECGPPHGPPTVSWWKDGKPLAQGRHTVSGSLLMARAKSDXT 177

Db 152 NVVAVGEPVAMECQPPRGHPPTISWKKDGSPDLDDKDERITIRGGKLMHSHTFKSDAGM 211

Qy 178 YMCVATNSAGHRESRAAR-VSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAE----- 229

Db 212 YMCVATNSAGHRESGAELVLERPSFURRPI-----NQVLADAPVNFCEVQG 261

Qy 230 GPKRPVAVLXWK 242

Db 262 DPQPN---LHWR 270

#### RESULT 4

T29549

hypothetical protein ZK377.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T29549

R;Nhan, M.; Hawkins, J.

submitted to the EMBL Data Library, February 1997

A;Description: The sequence of C. elegans cosmid ZK377.

A;Reference number: Z20639

A:Accession: T29549

A;Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-423 <NHA>

A;Cross-references: EMBL:U89183; PIDN:AAB52658.1; GSPDB:GN00028; CESP:ZK377.3

A;Experimental source: strain Bristol N2; clone ZK377

C:Genetics:

A:Gene: CESP:ZK377.3

A:Map position: X

A;Introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match

Best Local Similarity 34.0%; Score 354.5; DB 2; Length 423;

Matches 96; Conservative 44; Mismatches 101; Indels 41; Gaps 11;

Qy 5 PQILVHPDQQLFQCGPGPARMSCRASGPPPT--IRWLLNGQPL--SMVPPDPHLLPD-G 59

Db 30 PVIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWKDGPVITNKEQVNSHRIVLDTG 86

Qy 60 TLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFQIQPRDM 119

Db 87 SLFLKYNVSGKNGKD-----SDAGAYVCVANSHEGVEKSNESLKLAWLRDFEVRPRTV 141

Qy 120 VAVVGEQFTLECGPPHGPPTVSWWKDGKPLAQ--GRHTV--SGSLLMARAKSDXT 177

Db 142 QALGEMAVLECSPPRGFPFVSVWRKDKELRIQDMPRYTLHSDGNLIIDPVDERSGT 201

Qy 178 YMCVATNSAGHRESRAARVSI-----QBPQDYTEPVELLAVRIQLENTVLLNPDPAEG 230

Db 202 YQCVANNVNGERVSNPARLSVFKEPKPEQPKDMT-----VDVGAALVDFCRVTGD 252

Qy 231 PKRPPAVLXWKVSGPXELPNLTFPCSGPLPARELRGQR 272

Db 253 PQPQ-----ITWK-----RKNEPMFVTRAYIAKDNRLGLRIER 284

#### RESULT 5

T42405

sax-3 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000

C:Accession: T42405

R;Zallen, J.A.; Yi, B.A.; Bargmann, C.I.

Cell 92, 217-227, 1998

A;Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple asp

A;Reference number: Z22160; MUID:98117250; PMID:9458046

A:Accession: T42405

A;Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1273 <ZAL>

A;Cross-references: EMBL:AF041053; NID:g2804779; PIDN:AAC38848.1; PID:g2804780

C:Genetics:

A;Note: sax-3

C:Function:

A;Description: sax-3 function is required at the time of axon guidance

Query Match

Best Local Similarity 24.0%; Score 354.5; DB 2; Length 1273;

Matches 96; Conservative 44; Mismatches 101; Indels 41; Gaps 11;

Qy 5 PQILVHPDQQLFQCGPGPARMSCRASGPPPT--IRWLLNGQPL--SMVPPDPHLLPD-G 59

Db 31 PVIIEHPIDVVVSRGSPATLNC---GAKPSTAKITWKDGPVITNKEQVNSHRIVLDTG 87

Qy 60 TLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFQIQPRDM 119

Db 88 SLFLKLVNSGKNGKD-----SDAGAYCYVASNEHGEVNSKESGLKAMLREDFRVRPRTV 142  
Qy 120 VAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQP-GRHTV-SGSSLMARAEKSDXT 177  
Db 143 QALGEMAVLECSPPRGPEPVSWRKDKELRIQDMRYTLHSDGNLIIDPVDRSDSGT 202  
Qy 178 YNCVATNSAGHRESRAARVSI-----QEPDYTEPVELLAVRIQLENVTLNPPDPAEG 230  
Db 203 YQCVANNMVERVSNPABLSVPEKPKFEQPKDMT-----VDVGAAVLFDRCRVTD 253  
Qy 231 PKPRPAVVLXWVSGPXLPLNLTSCSPRLPREARELRGOR 272  
Db 254 PQPQ-----ITWK-----RXNEPMPVTRAYIAKONRGLRIER 285

RESULT 6  
S46224  
peroxidasein - fruit fly (*Drosophila* sp.)  
C:Species: *Drosophila* sp.  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Oct-2000  
A:Accession: S46224  
R:Neelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parker, E.M.B. J. Biol. Chem. 263:3447-3457, 1988  
A:Title: Peroxidasein: a novel enzyme-matrix protein of *Drosophila* development.  
A:Reference number: S46224; MUID:94341255; PMID:8062820  
A:Accession: S46224  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1535 <NE>  
A:Cross-references: G8:U1052; NID:9531384; PIDN:AAA61568.1; PID:9531385  
C:Superfamily: peroxidasein; myeloperoxidase homology; proteoglycan amino-terminal homology  
F:19-44/Domain: proteoglycan amino-terminal homology <PAH4>  
F:661-1350/Domain: myeloperoxidase homology <MPX>

Query Match 17.2%; Score 253; DB 2; Length 1535;  
Best Local Similarity 30.3%; Pred. No. 1.9e-11;  
Matches 80; Conservative 33; Mismatches 109; Indels 42; Gaps 13;

Qy 3 SPPQILVHPDQL--FQGGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
Db 367 SPPHTHPPHQIVAHLSGSHVLLDCAASGPPQDIQMFVNGRQLQSTPS-LQLQANGS 425  
Qy 61 LLLQPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPRDMV 120  
Db 456 LILLQP-----NQLSA--GTYRCEARNSLG-SVQATARIELKELPE-ILTPAQSGT 472  
Qy 121 AVVGQFTLECGPPWGHPEPTVSWKDGKPLALQP-----RHTVSGSSLMARAEKSD 175  
Db 473 IKLGKAFVLECDAD-GNPLPTIDMQLNGVPL---FGNTPDLQLENENTELVVGAAQOHA 528  
Qy 176 XYTCMVATNSAGHRESRAARVSIQ8-----PDYTEPVELLAV--RIQLENVTLNPPDPA 228  
Db 529 GYVRCVATNSAGHRESRAARVSIQ8-----PDYTEPVELLAV--RIQLENVTLNPPDPA 228  
Qy 229 EGKPRPAVVLXWVSGPXLPLNLTSCSPRLPREARELRGOR 252  
Db 579 QADQPEDGLQISWRHGRLLIDNV 602

RESULT 7  
S26180  
neurofascin - chicken  
C:Species: *Gallus gallus* (chicken)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
A:Accession: S26180  
R:Volkmann, H.; Hassel, B.; Wolff, J.M.; Frank, R.; Rathjen, F.G.  
J. Cell Biol. 118, 149-161, 1992  
A:Title: Structure of the axonal surface recognition molecule neurofascin and its relation to the cell adhesion molecule L1.  
A:Reference number: S26180; MUID:92317154; PMID:1377696  
A:Accession: S26180  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1272 <VOL>

A:Cross-references: EMBL:X65224; NID:963659; PIDN:CAA46330.1; PID:963660  
C:Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology;  
F:275-336/Domain: immunoglobulin homology <IMW>

Query Match 17.0%; Score 251; DB 2; Length 1272;  
Best Local Similarity 34.5%; Pred. No. 2.2e-11;  
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 5 PQILVHPDQLFQGGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGTLL 63  
Db 355 PYWLDEFQNL-LAPGEGDGLVCRANGPKSIOQLVNGEPIEGSPNPSREVAGDTIVF 413  
Qy 64 LPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLRDFQIQPR----- 117  
Db 414 -----RDTQIGSS--AVYQCVATNSAGHRESRAARVSIQ8-----ANAFVSVL---DVPRLILAPRN 455  
Qy 118 DMVAVGEOFT-LECGPPWGHPEPTVSWKDGKPLALQPGRHTV-SGSSLMARAEKSD 175  
Db 456 QLIKVIQNRRLDC-PFEGSPIPTLRWFKNGQGNLMDGGNYKAHENGSLMSMARKEDQ 514  
Qy 176 XYTCMVATNSAGHRESRAARVSIQ8 201  
Db 515 GIYTCVATNLGKVEAQ-VRLVKDP 539

RESULT 8  
S15169  
tumor suppressor - African clawed frog  
C:Species: *Xenopus laevis* (African clawed frog)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
A:Accession: S15169  
R:Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R.  
Dev. Biol. 166, 654-665, 1994  
A:Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the  
A:Reference number: S15169; MUID:95113183; PMID:7813784  
A:Accession: S15169  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1427 <PTE>  
A:Cross-references: EMBL:U10986; NID:9606873; PIDN:AAA70168.1; PID:9606874  
C:Genetics:  
A:Gene: XDCCA

Query Match 16.6%; Score 245; DB 2; Length 1427;  
Best Local Similarity 31.0%; Pred. No. 7.1e-11;  
Matches 75; Conservative 32; Mismatches 99; Indels 36; Gaps 10;

Qy 22 ARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLL-LPDGTLLLLQPPARGHAHQDQALST 80  
Db 157 ALLRCBITGEMPTISWQKNEEDLKVTPGDPRLVLPSTGLQI-----SRLQADG----- 207  
Qy 81 DLGVYTCEASNRGLGTAVSRGARLSVAVLRD-----FQIQPRDMVAVGEOFTLECGP 133  
Db 208 --GYVRCVATNSAGHRESRAARVSIQ8-----RILSESGLHQVQLQPRSNVVAIEGQDAVLECAV 263  
Qy 134 PWGHPEPTVSWKDGKPLALQPGRHTVSGGS-LLMARAEKSDXYTCMVATNSAGHRESR 192  
Db 264 S-GYPTTIIVWQGDPEVPITRKYSVLGSNLLISNVITDDAGAYTCVATYKNTSFS 322  
Qy 193 AARVSIQ8PDYTEPVELLA---VRIQLENVTLNPPDPAEGKPRPAVVLXWVSGPXL 249  
Db 323 ADLTVMPVPPQPLNHPANLYAVESMDIEFE-----CAVSGKPSPTV--KWTKNGEVVI 372  
Qy 250 PN 251  
Db 373 PS 374

RESULT 9  
S46216  
leukocyte antigen-related protein precursor - rat  
N:Alternate names: leukocyte common antigen homolog  
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)



C/Species: Rattus norvegicus (Norway rat)  
C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text\_change 23-Jul-1999  
C/Accession: S46216; S23252; A41032; A33154  
R/Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
Biochem. J. 302, 39-47, 1994  
A/Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase from rat liver  
A/Reference number: S46216; MUID:94347119; PMID:8068021  
A/Accession: S46216  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-1898 <ZHA>  
A/Cross-references: EMBL:L11586; NID:9205132; PIDN:AAC37655.1; PID:9205133  
R/Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
Biochem. J. 284, 569-576, 1992  
A/Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three different protein-tyrosine phosphatases  
A/Reference number: S23126; MUID:92287069; PMID:1599438  
A/Accession: S23126  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1361-1604; 1649-1898 <HAS>  
R/Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
J. Biol. Chem. 266, 19688-19696, 1991  
A/Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic region of the insulin receptor  
A/Reference number: A41032; MUID:92011772; PMID:1918076  
A/Accession: A41032  
A/Molecule type: mRNA  
A/Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
A/Cross-references: GB:M0103; NID:9205130; PIDN:AAM41510.1; PID:9205131  
R/Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
Submitted to the Protein Sequence Database, December 1990  
A/Reference number: A33154  
A/Accession: A33154  
A/Molecule type: mRNA  
A/Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
C/Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase  
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogg  
C/Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; tyrosine phosphatase  
F/1-26/Domain: (or 1-26) signal sequence #status predicted <SIG>  
F/28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT>  
F/28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>  
F/47-109/Domain: immunoglobulin homology <IMM1>  
F/149-209/Domain: immunoglobulin homology <IMM2>  
F/246-300/Domain: immunoglobulin homology <IMM3>  
F/413-499/Domain: fibronectin type III repeat homology <FN3A>  
F/511-593/Domain: fibronectin type III repeat homology <FN3B>  
F/606-695/Domain: fibronectin type III repeat homology <FN3C>  
F/708-799/Domain: fibronectin type III repeat homology <FN3D>  
F/811-895/Domain: fibronectin type III repeat homology <FN3E>  
F/906-990/Domain: fibronectin type III repeat homology <FN3F>  
F/1002-1079/Domain: fibronectin type III repeat homology <FN3G>  
F/1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>  
F/1276-1898/Domain: intracellular #status predicted <INT>  
F/1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F/1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F/1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F/154-107, 156-207, 253-298/Disulfide bonds: #status predicted  
F/117, 250, 295, 721, 957/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/1539/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F/1545/Binding site: substrate phosphate (Arg) #status predicted  
F/1830/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F/1836/Binding site: substrate phosphate (Arg) #status predicted

Db 86 GAGSVLRIQP-----LRVQDEAIYEECTATNSIG-EINTSAKLS--VLEEDQLPSG 133  
QY 112 ---FQIQPRDMVAVGEQFLGCGPPNGHPEPTVSWKCKPL--ALQPCR-HTVSGSL 165  
Db 134 FPTIDMGPLKVVKEKARTATMLCA-AGNPDPIBSWFKDPLVDPPASSNGRIKQLRSGAL 192  
QY 166 LMAAEKSDXTYCMVATNSAGHRSRAARVSQ 199  
Db 193 QIESSESQCKYECVATNSAGTRYAPANLYVR 226  
RESULT 10  
TDHULK  
leukocyte antigen-related protein precursor - human  
N/Alternate names: leukocyte common antigen homology  
N/Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
C/Accession: S03841; JLO051  
R/Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.  
J. Exp. Med. 168, 1523-1530, 1988  
A/Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the leukocyte antigen-related protein; fibronectin type III repeat homology;  
A/Reference number: JLO051; MUID:89035978; PMID:2972792  
A/Accession: S03841  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-1897 <STR>  
A/Cross-references: EMBL:Y00815; NID:934266; PIDN:CAA68754.1; PID:g34267  
C/Genetics:  
A/Gene: GDB:PTPRF; LAR  
A/Cross-references: GDB:120138; OMIM:179590  
A/Map position: lp34-lp34  
C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F/1-16/Domain: signal sequence #status predicted <SIG>  
F/17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>  
F/17-1250/Domain: extracellular #status predicted <EXT>  
F/37-99/Domain: immunoglobulin homology <IMM1>  
F/139-199/Domain: immunoglobulin homology <IMM2>  
F/236-290/Domain: immunoglobulin homology <IMM3>  
F/308-390/Domain: fibronectin type III repeat homology <FN3A>  
F/403-489/Domain: fibronectin type III repeat homology <FN3B>  
F/501-583/Domain: fibronectin type III repeat homology <FN3C>  
F/596-585/Domain: fibronectin type III repeat homology <FN3D>  
F/698-798/Domain: fibronectin type III repeat homology <FN3E>  
F/810-893/Domain: fibronectin type III repeat homology <FN3F>  
F/905-989/Domain: fibronectin type III repeat homology <FN3G>  
F/1001-1078/Domain: fibronectin type III repeat homology <FN3H>  
F/1251-1274/Domain: transmembrane #status predicted <TM>  
F/1251-1897/Domain: intracellular #status predicted <INT>  
F/1286-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F/1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F/1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F/44-97, 146-197, 243-288/Disulfide bonds: #status predicted  
F/107, 240, 285, 711, 956/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/1538/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F/1544/Binding site: substrate phosphate (Arg) #status predicted  
F/1829/Active site: Cys (phosphotyrosine intermediate) #status predicted  
F/1835/Binding site: substrate phosphate (Arg) #status predicted  
Query Match 15.8%; Score 232.5; DB 1; Length 1897;  
Best Local Similarity 31.6%; Pred. No. 8.9e-10;  
Matches 68; Conservative 37; Mismatches 75; Indels 35; Gaps 9;  
QY 2 DSPPQILVHPQDQLQFGPGPARMSCRASGQPPPTIRWLLNGQPLS-----MVPDPHLL 56  
Db 20 DSKPFFVKVEDQTLGSGVASFVQATGEPKPRI-TWKKGKVSORFVEIEDD---- 75  
QY 57 PDGTLILLQPPARGHAHDQALSTDLGVYTCESNRNLGTVASRGARLSVAVLRDFQIQP 116  
Db 76 GAGSVLRIQP-----LRVQDEAIYEECTATNSIG-EINTSAKLSVL---EEQLPP 122

A:Molecule type: mRNA  
A:Residues: 1-296,'T','298-1040 <HA>  
A:Cross-references: EMBL:X68274  
R:Tsiotra, P.C.; Karagozogs, D.; Theodorakis, K.; Michaelidis, T.M.; Modi, W.S.; Furley,  
Genomics 18, 562-567, 1993  
A:Title: Isolation of the cDNA and chromosomal localization of the gene (TAX1) encoding  
A:Reference number: A49356; MUID:94140354; PMID:8307567  
A:Accession: A49356  
A:Molecule type: mRNA  
A:Residues: 1-1001,'G','1003-1040 <TSI>  
A:Cross-references: GB:X67734  
C:Genetics:  
A:Gene: GDB:TAX; TAX1  
A:Cross-references: GDB:I38782  
A:Map position: lq32-lq32  
C:Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology  
C:Keywords: cell adhesion; glycoprotein  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:19-1040/Product: axonal glycoprotein TAG-1 #status predicted <MAT>  
F:254-308/Domain: immunoglobulin homology <IMM1>  
F:341-397/Domain: immunoglobulin homology <IMM2>  
F:76,138,204,461,477,498,525,775,830,904,918,940/Binding site: carbohydrate (Asn) (coval

Query March      15.5%; Score 228; DB 2; Length 1040;

Best Local Similarity    29.5%; Pred. No. 1e-09;

Matches    79; Conservative    38; Mismatches    99; Indels    52; Gaps    13;

Qy     1 QDSPPTLVHPFDQLFOFGPARMSCRASGPPTIRWLLNQPLSMVPPDPHLLPDGT 60  
     : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     40 EDQP LSVL - FEESTEE --- QVLLACRARASPATVRWKMGTEMKLGPSRHOLV-GGN 94  
  
Qy     61 LLLLQPPARGHAHQDALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFQLQRDMV 120  
     : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     95 LVINMP -----TKRADAGVTQCILNASNPVGTVSREAILRFGLQE-FSKERDVP 143  
  
Qy     121 -VVGEQTLECGPWGHPEPVSMDCKPLAL-QPGRTYS--GGSLMARAEKSDEX 176  
     : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     144 KAHEGWGMUPCNPAHYPLGSRYRMELNEFPNPFIDGRHRFSVQTTGNLYARTNASDLG 203  
  
Qy     177 TYMCVATNSAGR-----SRAARVSIQ-----EPQDYTEPVPELLAVRIQE 218  
     : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     204 NYSCLATS---HMDFSTKSVSKFAQLNLAAEDTRLFPSIKARPPAETVALVCQQVTL 260  
  
Qy     219 NVTLNLPDAEGPKPRPAWLXW-KVSG 245  
     ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :  
Db     261 CFARFNVP R-----IKWRKV DG 278

RESULT 13

T20992  
hypothetical protein F15G9.4a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T20992; T24733  
R:Sulston, J.  
submitted to the EMBL Data Library, December 1994  
A:Reference number: Z19355  
A:Accession: T20992  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-5175 <ML>  
A:Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a  
A:Experimental source: Clone F15G9  
R:Kershaw, J.  
submitted to the EMBL Data Library, December 1994  
A:Reference number: Z19929  
A:Accession: T24733  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-5175 <MT2>  
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a  
A:Experimental source: clone T09B9  
C:Genetics:

A:Gene: CESP:F15G9.4a  
A:Map position: X  
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;  
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;  
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1;  
Query Match 15.5%; Score 228; DB 2; Length 5175;  
Best Local Similarity 28.6%; Pred. No. 6e-09;  
Matches 74; Conservative 35; Mismatches 104; Indels 46; Gaps 10;  
QY 4 PPQILVHPDQLFGP--GPARMSCRASGQPPPTIRMLNGOPLSMVPPDPHLLPDGTL 61  
DB 3216 PPRI--EDEERVLOGKEGNTVMHCQVTPVYVTKRNGKEIQENP----- 3262  
QY 62 LLLQPPARGHAGDQALSTDLGVVTCESNRLGTAVSRGARGLSVAVL-REDFOIQPRDMV 120  
DB 3263 -----VLHNRNATRADGKYSCLASNEAGTAV---ADFLIDVFTKPTFETHETTFN 3310  
QY 121 AVVGEQFTLECGPPWGHPEPTVSMWKGKPLALQPGRHVTSGSLLMARAKSDEXTYMC 180  
DB 3311 IVEGESAKIECKID-GHPKPTISMLKGRPFNMNDIILSPRGDTLMILKAQRFDDGLYTC 3369  
QY 181 VATNSAGHRE-----SRAARVSIQEPDYTEPVELLAVRIQLENVTLNPPAPSGPKRPP 235  
DB 3370 VATNSYGDSDQDFKVNVTKYPIDETIDQT-PKAVAGGEIILKCPVLGNPTPT----- 3421  
QY 236 AVMLXKVKVSGPXRPLNLR 254  
DB 3422 ---VTWK-RGDDAVPNSR 3436  
RESULT 14  
T43290  
hemocentin precursor - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T43290; T20993; T24734  
R:Vogel, B.E.; Hedgecock, E.M.  
submitted to the EMBL Data Library, June 1998  
A:Description: Hemocentin is required for hemidesmosome mediated cell adhesion and germ-  
A:Reference number: Z22396  
A:Accession: T43290  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5198 <VOG>  
A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1  
R:Sulston, J.  
submitted to the EMBL Data Library, December 1994  
A:Reference number: Z19355  
A:Accession: T20993  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5198 <WIL>  
A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b  
A:Experimental source: clone F15G9  
R:Kershaw, J.  
submitted to the EMBL Data Library, December 1994  
A:Reference number: Z19929  
A:Accession: T24734  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5198 <W12>  
A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b  
A:Experimental source: clone T09B9  
C:Genetics:  
A:Gene: him-4; F15G9.4b  
A:Map position: X  
A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;  
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;  
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1;  
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Best Local Similarity 28.6%; Pred. No. 6.1e-09;

Matches 74; Conservative 35; Mismatches 104; Indels 46; Gaps 10;  
QY 4 PPQILVHPDQLFGP--GPARMSCRASGQPPPTIRMLNGOPLSMVPPDPHLLPDGTL 61  
DB 3216 PPRI--EDEERVLOGKEGNTVMHCQVTPVYVTKRNGKEIQENP----- 3262  
QY 62 LLLQPPARGHAGDQALSTDLGVVTCESNRLGTAVSRGARGLSVAVL-REDFOIQPRDMV 120  
DB 3263 -----VLHNRNATRADGKYSCLASNEAGTAV---ADFLIDVFTKPTFETHETTFN 3310  
QY 121 AVVGEQFTLECGPPWGHPEPTVSMWKGKPLALQPGRHVTSGSLLMARAKSDEXTYMC 180  
DB 3311 IVEGESAKIECKID-GHPKPTISMLKGRPFNMNDIILSPRGDTLMILKAQRFDDGLYTC 3369  
QY 181 VATNSAGHRE-----SRAARVSIQEPDYTEPVELLAVRIQLENVTLNPPAPSGPKRPP 235  
DB 3370 VATNSYGDSDQDFKVNVTKYPIDETIDQT-PKAVAGGEIILKCPVLGNPTPT----- 3421  
QY 236 AVMLXKVKVSGPXRPLNLR 254  
DB 3422 ---VTWK-RGDDAVPNSR 3436  
RESULT 15  
S18252  
heparan sulfate proteoglycan - mouse  
N:Alternate names: perlecan  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S18252; A31917; B31917; S66460  
R:Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha  
J. Biol. Chem. 266, 22939-22947, 1991  
A:Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly  
adhesion molecule.  
A:Reference number: S18252; MUID:92078153; PMID:1744087  
A:Accession: S18252  
A:Molecule type: mRNA  
A:Residues: 1-3707 <NOO>  
A:Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296  
R:Noonan, D.M.; Horigan, E.A.; Lebetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass  
J. Biol. Chem. 263, 16379-16387, 1988  
A:Title: Identification of cDNA clones encoding different domains of the basement membra  
A:Reference number: A92680; MUID:89034110; PMID:2972708  
A:Accession: A31917  
A:Molecule type: mRNA  
A:Residues: 940-1601 <NO2>  
A:Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253  
A:Accession: B31917  
A:Molecule type: mRNA  
A:Residues: 1870-2600 <NO3>  
A:Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301  
R:Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.  
Eur. J. Biochem. 231, 551-556, 1995  
A:Title: Structural properties of recombinant domain III-3 of perlecan containing a glob  
A:Reference number: S66460; MUID:95377282; PMID:7649154  
A:Accession: S66460  
A:Molecule type: protein  
A:Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>  
C:Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repe  
C:Keywords: Glycoprotein  
F:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F:764-811/Domain: laminin-type EGF-like homology <LEG>  
F:1159-1206/Domain: laminin-type EGF-like homology <LEG7>  
F:1563-1610/Domain: laminin-type EGF-like homology <EG7>  
F:1613-1668/Domain: laminin-type EGF-like homology <LEG8>  
F:3163-3198/Domain: EGF homology <EGF>  
F:3270-3423/Domain: laminin G repeat homology <LG2>  
F:3464-3492/Domain: EGF homology <EGF7>  
F:1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.3%; Score 225; DB 2; Length 3707;  
Best Local Similarity 27.6%; Pred. No. 7.1e-09;  
Matches 72; Conservative 37; Mismatches 86; Indels 66; Gaps 13;

Qy	4	PPQILVHPQDQLFOGPGPARM-----SCRASQPPPTIRWLLNGOPLSMVP-----PDP	52
Db	2433	PPTVSVP-----EGPVHVGMKDTLECISSGEPRSSPRWTRLGIPVKLEPRMFLMNS	2487
Qy	53	HLLPDGTLILLQPPARGHAHDGOALSTDLYVTCEASNRLGTA-----VSRGARLSV	105
Db	2488	HAML---KIASVKP-----SDAGTYVCOAQNALGTAQKQVELIYDTG---TV	2528
Qy	106	AVLREDFQIOPRDMVAVVGEQTECGPPWHPEPTVSWKDGKPLALOPGRHTVSGSL	165
Db	2529	APGTFQVQVESELTEAGHTATLHCSAT-GNPPPTIHWKLRAPL---PMQHRIEGNTL	2584
Qy	166	LMAAEKSDXTYMCVATNSAGHRESRAARVSIQRPQDYT-----EPVELLAVRIOL	217
Db	2585	VIPRVAQQSQGYICNATNSAGHTATVV-LHVESPPYATIIPEHTSAQPGNL-----VOL	2639
Qy	218	ENVTLINPDPAEGPKPRPAVW	238
Db	2640	QCL-----AHGTPPLTYQW	2653

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Job time : 14.3472 secs

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DR SMART; SM00200; SEA; 1.  
DR PROSITE; PS00022; EGF 1; 9.  
DR PROSITE; PS01186; EGF 2; 6.  
DR PROSITE; PS08835; IG-LIKE; 22.  
DR PROSITE; PS00025; LAM G DOMAIN; 3.  
DR PROSITE; PS01248; LAMININ TYPE EGF; 11.  
DR PROSITE; PS01209; LDLRA 1; 4.  
DR PROSITE; PS00068; LDLRA 2; 4.  
DR PROSITE; PS00024; SEA; 1.  
KW Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;  
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;  
KW Extracellular matrix; EGF-like domain; Disease mutation.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 4391 SULFATE PROTEOGLYCAN CORE PROTEIN.  
FT DOMAIN 80 194 SEA.  
FT DOMAIN 198 235 LDL-RECEPTOR CLASS A 1.  
FT DOMAIN 284 320 LDL-RECEPTOR CLASS A 2.  
FT DOMAIN 324 360 LDL-RECEPTOR CLASS A 3.  
FT DOMAIN 367 404 LDL-RECEPTOR CLASS A 4.  
FT DOMAIN 405 504 IG-LIKE C2-TYPE 1.  
FT DOMAIN 521 530 LAMININ EGF-LIKE 1 (N-TERMINAL).  
FT DOMAIN 531 730 LAMININ DOMAIN IV 1 (DOMAIN III A).  
FT DOMAIN 731 763 LAMININ EGF-LIKE 1 (C-TERMINAL).  
FT DOMAIN 764 813 LAMININ EGF-LIKE 2.  
FT DOMAIN 814 871 LAMININ EGF-LIKE 3.  
FT DOMAIN 879 923 LAMININ EGF-LIKE 4 (INCOMPLETE).  
FT DOMAIN 924 933 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 934 1125 LAMININ DOMAIN IV 2 (DOMAIN III B).  
FT DOMAIN 1126 1158 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 1159 1208 LAMININ EGF-LIKE 6.  
FT DOMAIN 1209 1265 LAMININ EGF-LIKE 7.  
FT DOMAIN 1275 1324 LAMININ EGF-LIKE 8.  
FT DOMAIN 1325 1334 LAMININ EGF-LIKE 9 (N-TERMINAL).  
FT DOMAIN 1335 1329 LAMININ DOMAIN IV 3 (DOMAIN III C).  
FT DOMAIN 1530 1562 LAMININ EGF-LIKE 9 (C-TERMINAL).  
FT DOMAIN 1563 1612 LAMININ EGF-LIKE 10.  
FT DOMAIN 1613 1670 LAMININ EGF-LIKE 11.  
FT DOMAIN 1677 1771 IG-LIKE C2-TYPE 2.  
FT DOMAIN 1772 1865 IG-LIKE C2-TYPE 3.  
FT DOMAIN 1866 1955 IG-LIKE C2-TYPE 4.  
FT DOMAIN 1956 2051 IG-LIKE C2-TYPE 5.  
FT DOMAIN 2052 2151 IG-LIKE C2-TYPE 6.  
FT DOMAIN 2152 2244 IG-LIKE C2-TYPE 7.  
FT DOMAIN 2245 2340 IG-LIKE C2-TYPE 8.  
FT DOMAIN 2341 2436 IG-LIKE C2-TYPE 9.  
FT DOMAIN 2437 2533 IG-LIKE C2-TYPE 10.  
FT DOMAIN 2534 2629 IG-LIKE C2-TYPE 11.  
FT DOMAIN 2630 2726 IG-LIKE C2-TYPE 12.  
FT DOMAIN 2727 2826 IG-LIKE C2-TYPE 13.  
FT DOMAIN 2827 2924 IG-LIKE C2-TYPE 14.  
FT DOMAIN 2925 3021 IG-LIKE C2-TYPE 15.  
FT DOMAIN 3022 3112 IG-LIKE C2-TYPE 16.  
FT DOMAIN 3113 3211 IG-LIKE C2-TYPE 17.

Query Match 13.8%; Score 203.5; DB 1; Length 4391;  
Best Local Similarity 26.5%; Pred. No. 9.4e-08;  
Matches 68; Conservative 38; Mismatches 114; Indels 37; Gaps 9;  
QY 4 PPQILVHPDQQLFQSGGPA-RMSCASGQPPPTIRWLNGQPLSNVPPDPHLLPDGTL 62  
DB 3111 PPTVSLPEGPVWVKVKAIVLECVSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVL 3170  
QY 63 LQPPARGHAGDQALSTDLGYTCEASNRGLTA-----VSRCARLSVAVLREDFOIQ 115  
DB 3171 QI-----SSAKPSDAGTYVCLAQNALGTAKQVEVIVDTGA---MAPGAPQVQAE 3217  
QY 116 PRDMVAVVGEQFTLECGPPGWPPEPTVSWKDGKPLALQPGRHTVSGGSLLMARAEKSD 175  
DB 3218 EAEVLVEAGHTATLRCSAT-GSPATIHWSKLRSL---PWQHRLEGDTLIIIPVAQODS 3273  
QY 176 XYTMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVR-----IQLENVTLNLPDPAEGP 231

Db 3274 GQYICNATSPAGHAEATII-LHVESPPYATTVPHEASVQAGETVQLQCL-----AHGT 3325  
QY 232 KRPAPAVLXWKVSGPXR 248  
Db 3326 PPLTFQMSRVGSSLFGR 3342  
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Job time : 10.5337 secs

PGSM\_HUMAN STANDARD; PRT; 4391 AA.  
P98160; Q16287; Q9H3V5;  
01-OCT-1996 (Rel. 34, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
15-SEP-2003 (Rel. 42, Last annotation update)  
DE Basement membrane-specific heparan sulfate proteoglycan core  
GN protein precursor (HSPG) (Perlecan) (PLC).  
HSPG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=92112994; PubMed=1730768;  
RA Kallunki P., Tryggvason K.;  
RT "Human basement membrane heparan sulfate proteoglycan core protein: a  
RT 467-kD protein containing multiple domains resembling elements of the  
RT low density lipoprotein receptor, laminin, neural cell adhesion  
RT molecules, and epidermal growth factor.";  
RL J. Cell Biol. 116:559-571(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon, and Skin;  
RX MEDLINE=92235084; PubMed=1569102;  
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;  
RT "Primary structure of the human heparan sulfate proteoglycan from  
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple  
RT domains homologous to the low density lipoprotein receptor, laminin,  
RT neural cell adhesion molecules, and epidermal growth factor.";  
RL J. Biol. Chem. 267:8544-8557(1992).  
RN [3]  
RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.  
RX MEDLINE=20553141; PubMed=1101850;  
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,  
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,  
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,  
RA Hentati F., Fontaine B.;  
RT "Perlecan, the major proteoglycan of basement membranes, is altered in  
RT patients with Schwartz-Jampel syndrome (Chondrodysplastic myotonia).";  
RL Nat. Genet. 26:480-483(2000).  
RN [4]  
RP SEQUENCE OF 1016-1470 FROM N.A.  
RC TISSUE=Colon;  
RX MEDLINE=91365376; PubMed=1679749;  
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,  
RA Yi H.F., Iozzo R.V.;  
RT "Heparan sulfate proteoglycan of human colon: partial molecular  
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the  
RT short arm of human chromosome 1.";  
RL Genomics 10:673-680(1991).  
RN [5]  
RP SEQUENCE OF 890-1396 FROM N.A.  
RC TISSUE=Fibroarcoma;  
RX MEDLINE=92120660; PubMed=1685141;  
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,  
RA Tryggvason K.;  
RT "Cloning of human heparan sulfate proteoglycan core protein,  
RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of  
RT a BamHI restriction fragment length polymorphism.";  
RL Genomics 11:389-396(1991).  
RN [6]  
RP SEQUENCE OF 1-21 FROM N.A.  
RX MEDLINE=94052171; PubMed=8234307;  
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;  
RT "Structural characterization of the complete human perlecan gene and  
RT its promoter.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).  
CC -!- FUNCTION: This protein is an integral component of basement  
CC membranes. It is responsible for the fixed negative electrostatic  
CC charge and is involved in the charge-selective ultrafiltration  
CC properties. It serves as an attachment substrate for cells.  
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in

dimers or stellate structures. It interacts with other basement  
membrane components such as laminin, prolargin and collagen type  
IV.  
-!- SUBCELLULAR LOCATION: Extracellular.  
-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.  
-!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED  
AND O-LINKED OLIGOSACCHARIDES.  
-!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel  
syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder  
characterized by permanent myotonia (prolonged failure of muscle  
relaxation) and skeletal dysplasia, resulting in reduced stature,  
kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.  
-!- SIMILARITY: Contains 4 LDL-receptor class A domains.  
-!- SIMILARITY: Contains 11 laminin EGF-like domains.  
-!- SIMILARITY: Contains 3 laminin IV domains.  
-!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.  
-!- SIMILARITY: Contains 3 laminin G-like domains.  
-!- SIMILARITY: Contains 4 EGF-like domains.  
-!- SIMILARITY: Contains 1 SEA domain.  
-----  
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between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; X62515; CAA44373.1; -;  
DR EMBL; M85289; AAA52700.1; -;  
DR EMBL; AL445795; CAC18534.1; -;  
DR EMBL; M64283; AAA52699.1; -;  
DR EMBL; S76436; AAB21121.2; -;  
DR EMBL; L22078; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A38096; A38096.  
DR HSSP; P00740; 1EDM.  
DR Sienna-2DPAGE; P98160; -;  
DR Genew; HGNC:5273; HSPG2.  
DR MIM; 142461; -;  
DR MIM; 255800; -;  
DR GO; GO:0005206; F:heparin sulfate proteoglycan; TAS.  
DR InterPro; IPR00742; EGF\_2.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR006210; EGF.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003598; Ig\_C2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR InterPro; IPR000034; Laminin\_B.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR002172; LDL\_receptor\_A.  
DR InterPro; IPR000082; SEA\_domain.  
DR Pfam; PF00008; EGF\_4.  
DR Pfam; PF00047; Ig\_22.  
DR Pfam; PF00052; laminin\_B; 3.  
DR Pfam; PF00053; laminin\_EGF; 7.  
DR Pfam; PF00054; laminin\_G; 3.  
DR Pfam; PF00057; ldl\_recept\_a; 4.  
DR Pfam; PF01390; SEA\_1.  
DR PRINTS; PR00010; EGFBL00D.  
DR PRINTS; PR00261; LDLRECEPTOR.  
DR ProDom; PD003031; Laminin\_B; 3.  
DR SMART; SM00181; EGF; 15.  
DR SMART; SM00180; EGF\_Lam; 12.  
DR SMART; SM00409; IG\_22.  
DR SMART; SM00408; IGC2; 21.  
DR SMART; SM00406; IGV; 7.  
DR SMART; SM00281; LamB; 3.  
DR SMART; SM00282; LamG; 3.  
DR SMART; SM00192; LDLa; 4.





RC TISSUE=Brain;  
RX MEDLINE=97407661; PubMed=9264410;  
RA Keeling S.L., Gad J.M., Cooper H.M.;  
RT "Mouse neogenin, a DC-like molecule, has four splice variants and is  
expressed widely in the adult mouse and during embryogenesis.";  
RL Oncogene 15:691-700(1997).  
CC -!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE  
TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR  
CC DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION  
CC MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=5;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1;  
CC IsoId=P97798-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P97798-2; Sequence=VSP\_002594;  
CC Name=3;  
CC IsoId=P97798-3; Sequence=VSP\_002595;  
CC Note=Expression developmentally regulated;  
CC Name=4;  
CC IsoId=P97798-4; Sequence=VSP\_002596;  
CC Note=Expression developmentally regulated;  
CC Name=5;  
CC IsoId=P97798-5; Sequence=VSP\_002597;  
CC Note=Expression developmentally regulated;  
CC -!- TISSUE SPECIFICITY: Widely expressed.  
CC -!- DEVELOPMENTAL STAGE: EXPRESSED UBQUITOUSLY THROUGHOUT THE MID TO  
LATE STAGES OF GESTATION AND IN ADULT TISSUES. STRONG EXPRESSION  
CC IS OBSERVED IN THE VENTRAL REGION OF THE VENTRICULAR ZONE OF THE  
CC E15.5 MOUSE NEURAL TUBE. AS WELL AS IN THE VENTRICULAR ZONES OF  
CC THE MESENCEPHALON AND RHOMBENCEPHALON. ISOFORMS 3 AND 4 ARE  
CC EXPRESSED AT HIGHER LEVEL COMPARED TO OTHER ISOFORMS BETWEEN E11.5  
CC AND E16.5.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC  
SUBFAMILY.  
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; Y09535; CAA70727.1; -.  
CC HSP; P02751; 1TTF.  
DR MGD; MGI:1097159; Neol.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003962; FN.III\_subd.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig C2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00041; fn3; 6.  
DR Pfam; PF00047; Ig; 4.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00060; FN3; 6.  
DR SMART; SM00408; IGC2; 4.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;  
KW Glycoprotein; Alternative splicing.  
FT SIGNAL 1 36  
FT CHAIN 37 1493  
FT DOMAIN 37 1136  
FT TRANSMEM 1137 1157  
FT DOMAIN 1158 1493  
FT DOMAIN 63 158  
FT DOMAIN 163 249  
FT DOMAIN 254 347  
FT DOMAIN 352 437

FT	DOMAIN	467	564	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	567	660	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	561	760	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	766	860	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	881	981	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	982	1083	FIBRONECTIN TYPE-III 6.
FT	DOMAIN	1149	1153	POLY-VAL.
FT	DISULFID	85	140	BY SIMILARITY.
FT	DISULFID	184	232	BY SIMILARITY.
FT	DISULFID	271	331	BY SIMILARITY.
FT	DISULFID	383	421	BY SIMILARITY.
FT	CARBOHYD	84	84	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	221	221	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	501	501	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	520	520	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	746	746	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	940	940	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	442	461	Missing (in isoform 2). /FTid=VSP_002594.
FT	VARSPLIC	863	878	Missing (in isoform 3). /FTid=VSP_002595.
FT	VARSPLIC	1086	1096	Missing (in isoform 4). /FTid=VSP_002596.
FT	VARSPLIC	1279	1331	Missing (in isoform 5). /FTid=VSP_002597.
SQ	SEQUENCE	1493 AA;	163159 MW;	441DE919D5E17C0E CRC64;

Query Match 14.2%; Score 209; DB 1; Length 1493;  
Best Local Similarity 29.5%; Pred. No. 1e-08;  
Matches 64; Conservative 32; Mismatches 99; Indels 22; Gaps 6;

Qy	3	SPPOILVHPDQLFQGGPGPARMSCRASGQPPPTIRLLNGQLPLSMVPPDPHLLPDGTL 62
Db	62	TPFYFLVPEVDTLVSRGSSVILNCAYSERSPNIEWKDGFTLNLESDRRQLPDGSLF 121
Qy	63	LLQPPARGCHADGQALSTDLGVYTCAS-NRLGTAVSARGAELSVAVLREDFQIQPRDVA 121
Db	122	ISNVVHSHKN-----KPDGFGYQCVATVNDLNGTIVSTAKTLVAGLPR-FTSQPEPSSV 174
Qy	122	VVGRQFTLEGPPMGHPE-----PTVSWKDGKPLALQPGRHVTVSGSLMLMAAEKSD 175
Db	175	YVGNSSALINC-----EVNADLVFVRWEQNRQPLLLDDRIVKLPSGTLVISNATEGDG 227
Qy	176	XTYMCVATNSAGHRESRAARVSI-QEPQDYTEPVVELL 211
Db	228	GLYRCIVESGGPPKFSDEALKVLQDPEEIVDLVFLM 264

RESULT 14  
DCC HUMAN  
ID - DCC HUMAN STANDARD; PRT; 1447 AA.  
AC P43146;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tumor suppressor protein DCC precursor (Colorectal cancer suppressor).  
GN DCC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95011532; PubMed=7926722;  
RA Hedrick L., Cho K.R., Fearon E.R., Wu T.-C., Kinzler K.W.,  
RA Vogelstein B.;  
RT "The DCC gene product in cellular differentiation and colorectal  
tumorigenesis.";  
RL Genes Dev. 8:1174-1183(1994).  
RN [2]  
RP SEQUENCE OF 1-750 FROM N.A.

DCC\_MOUSE  
ID - DCC\_MOUSE STANDARD; PRT; 1447 AA.  
AC P70211;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tumor suppressor protein DCC precursor.  
GN DCC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBITaxID=10090;  
RN [1]  
RC SEQUENCE FROM N.A. (ISOFORMS A; B AND C).  
RC STRAIN=BALB/c; TISSUE=Brain;  
RX MEDLINE=96112625; PubMed=8570174;  
RA Cooper H.M., Ames P., Britto J., Gad J., Wilke A.F.;  
RT "Cloning of the mouse homologue of the deleted in colorectal cancer  
RT gene (mDCC) and its expression in the developing mouse embryo.";  
RL Oncogene 11:2243-2254(1995).  
RN [2]  
RP REVISIONS.  
RC STRAIN=BALB/c; TISSUE=Brain;  
RA Cooper H.M.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=A;  
CC IsoId=p70211-1; Sequence=Displayed;  
CC Note=Isoform B is produced by alternative initiation at Met-85  
CC of isoform A;  
CC Name=C;  
CC IsoId=p70211-2; Sequence=VSP\_002501;  
CC Event=Alternative initiation;  
CC Comment=2 isoforms, A (shown here) and B, are produced by  
CC alternative initiation at Met-1 and Met-85;  
CC -!- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE  
CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN  
CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.  
CC ISOFORM C IS EXPRESSED ONLY IN THE EMBRYO.  
CC -!- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS  
CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION  
CC AND REMAIN AT THIS LEVEL IN THE ADULT.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC  
CC SUBFAMILY.  
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.  
-----  
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-----  
DR EMBL; X85788; CAA59786.1; -.  
DR HSSP; P56276; ITUK.  
DR MGD; MGI:94869; DCC.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR007110; Ig-Like.  
DR InterPro; IPR003598; Ig\_C2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00041; fn3; 6.  
DR Pfam; PF00047; Ig; 4.  
DR PRINTS; PR00014; FNTPYPIII.  
DR SMART; SM00060; FN3; 6.  
DR SMART; SM00408; IGC2; 3.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;

Repeat; Anti-oncogene; Alternative initiation; Alternative splicing.  
KW SIGNAL 1 25  
FT CHAIN 26 1447  
FT CHAIN 85 1447  
FT INIT\_MET 85 85  
FT DOMAIN 26 1097  
FT TRANSMEM 1098 1122  
FT DOMAIN 1123 1447  
FT DOMAIN 36 135  
FT DOMAIN 139 229  
FT DOMAIN 234 326  
FT DOMAIN 331 416  
FT DOMAIN 426 522  
FT DOMAIN 525 618  
FT DOMAIN 619 716  
FT DOMAIN 722 816  
FT DOMAIN 840 940  
FT DOMAIN 941 1042  
FT DISULFID 61 117  
FT DISULFID 161 212  
FT DISULFID 261 310  
FT DISULFID 352 400  
FT CARBOHYD 60 60  
FT CARBOHYD 94 94  
FT CARBOHYD 299 299  
FT CARBOHYD 318 318  
FT CARBOHYD 478 478  
FT CARBOHYD 628 628  
FT CARBOHYD 702 702  
FT CARBOHYD 819 838  
FT VARSPLIC  
FT SQ SEQUENCE 1447 AA; 158298 MW; ODIF1097C22DSB9F CRC64;  
Query Match 14.2%; Score 209; DB 1; Length 1447;  
Best Local Similarity 27.7%; Pred. No. 9.6e-09;  
Matches 67; Conservative 37; Mismatches 98; Indels 40; Gaps 10;  
Qy 24 MSCRASQPPPTIRWLINGQPLSNVPPDPH-HLLPDGTLILL--LQPPARGHAHDGQALST 80  
Db 159 LKCEVIGEPPTTHWKNQDNLPLGDSRVVLPSCALQISRLQP-----G 205  
Qy 81 DLGYTCEANRLGTAVSRCARLSAVLRD-----FQIPRDMVAVGGEQTFLEGGP 133  
Db 206 DSGYRCSARN--PASIRTGNEAEVRILSDPGLHRQLYFLQPSNVIAIEGKDAVLECCV 263  
Qy 134 PWGHPPTVSMWKGKPLALQGRHTVSGGS-LLMARAESDXYTMCVATNSAGHRESR 192  
Db 264 S-GYPPSPFTWLGRGEEVIQSRKKYSLGGSNLLISNVTDDSGTTCVVTYKKNISAS 322  
Qy 193 AARVSIQEPQDYTEPPVELLA---VRIQLENVTLINPDPAEGPKPRPAVWLXWKVSGPKRL 249  
Db 323 AELTVLVPFPFLNHPNSNLXAVESMDIEFE-----CAVSGKPVPTV--NMKNQGDVVI 372  
Qy 250 PN 251  
Db 373 PS 374  
RESULT 13  
NEOI\_MOUSE  
ID NEOI\_MOUSE STANDARD; PRT; 1493 AA.  
AC P97798;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Neogenin precursor.  
GN NEOI OR NGN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBITaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon carcinoma, and Placenta;  
RX MEDLINE=96074849; PubMed=7478540;  
RA Mossie K., Jallal B., Alves P., Sures I., Plozman G.D., Ullrich A.;  
RT "Colon carcinoma kinase-4 defines a new subclass of the receptor  
RT tyrosine kinase family.";  
RL Oncogene 11:2179-2184(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroblast;  
RX MEDLINE=97037064; PubMed=8882711;  
RA Park S.-K., Lee H.-S., Lee S.-T.;  
RT "Characterization of the human full-length PTK7 cDNA encoding a  
RT receptor protein tyrosine kinase-like molecule closely related to  
RT chick KLG.";  
RL J. Biochem. 119:235-239(1996).  
RN [3]  
RP SEQUENCE FROM N.A., AND REVISION TO 834.  
RA Lee S.-T., Park S.-K., Lee H.-S., Ji A.R., Jung J.W.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY  
CC THE CATALYTIC ACTIVITY OF TYROSINE KINASE. MAY BE CONNECTED TO THE  
CC PATHOPHYSIOLOGY OF COLON CARCINOMAS AND/OR MAY REPRESENT A TUMOR  
CC PROGRESSION MARKER.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, PANCREAS,  
CC KIDNEY, PLACENTA AND MELANOCYTES. WEAKLY EXPRESSED IN THYROID  
CC GLAND, OVARY, BRAIN, HEART AND SKELETAL MUSCLE. ALSO EXPRESSED IN  
CC ERTHROLEUKEMIA CELLS. BUT NOT EXPRESSED IN COLON.  
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN  
CC RECEPTOR SUBFAMILY.  
CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
CC -----  
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CC -----  
DR EMBL; U33635; AA87565.1; -.  
DR EMBL; U40271; AAC50484.2; -.  
DR EMBL; AF447176; AAL39062.1; -.  
DR EMBL; AF447157; AAL39062.1; JOINED.  
DR EMBL; AF447158; AAL39062.1; JOINED.  
DR EMBL; AF447162; AAL39062.1; JOINED.  
DR EMBL; AF447164; AAL39062.1; JOINED.  
DR EMBL; AF447167; AAL39062.1; JOINED.  
DR EMBL; AF447170; AAL39062.1; JOINED.  
DR EMBL; AF447171; AAL39062.1; JOINED.  
DR EMBL; AF447173; AAL39062.1; JOINED.  
DR EMBL; AF447174; AAL39062.1; JOINED.  
DR EMBL; AF447175; AAL39062.1; JOINED.  
DR HSSP; P08631; IAD5.  
DR Genew; HGNC:9618; PTK7.  
DR MIM; 601830; -.  
DR GO; GO:0005886; C:plasma membrane; TAS.  
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.  
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002011; RTK\_kinaseII.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00047; ig; 7.

DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PD00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00408; IGc2; 5.  
DR SMART; SM00219; Tyrcg; 1.  
DR PROSITE; PS00835; IG\_LIKE; 7.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
DR PROSITE; PS00239; RECEPTOR TYR\_KIN\_II; FALSE NEG.  
KW Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;  
KW Immunoglobulin domain; Repeat.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 1070 TYROSINE-PROTEIN KINASE-LIKE 7.  
FT DOMAIN 31 704 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 705 725 POTENTIAL.  
FT DOMAIN 726 1070 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 31 120 IG-LIKE C2-TYPE 1.  
FT DOMAIN 128 218 IG-LIKE C2-TYPE 2.  
FT DOMAIN 225 317 IG-LIKE C2-TYPE 3.  
FT DOMAIN 309 407 IG-LIKE C2-TYPE 4.  
FT DOMAIN 412 497 IG-LIKE C2-TYPE 5.  
FT DOMAIN 503 586 IG-LIKE C2-TYPE 6.  
FT DOMAIN 578 680 IG-LIKE C2-TYPE 7.  
FT DOMAIN 796 1066 PROTEIN KINASE; INACTIVE.  
FT DISULFID 53 101 BY SIMILARITY.  
FT DISULFID 150 200 BY SIMILARITY.  
FT DISULFID 246 301 BY SIMILARITY.  
FT DISULFID 343 391 BY SIMILARITY.  
FT DISULFID 433 481 BY SIMILARITY.  
FT DISULFID 524 570 BY SIMILARITY.  
FT DISULFID 613 664 BY SIMILARITY.  
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 175 175 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 646 646 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 92 92 K -> R (IN REF. 2 AND 3).  
FT CONFLICT 147 147 P -> T (IN REF. 2 AND 3).  
FT CONFLICT 207 207 S -> G (IN REF. 2 AND 3).  
FT CONFLICT 495 496 VL -> RV (IN REF. 2 AND 3).  
FT CONFLICT 515 515 G -> E (IN REF. 2 AND 3).  
FT CONFLICT 881 881 E -> G (IN REF. 2 AND 3).  
FT CONFLICT 969 969 A -> P (IN REF. 2 AND 3).  
FT CONFLICT 992 992 S -> F (IN REF. 2 AND 3).  
SQ SEQUENCE 1070 AA; 118260 MW; 47CDF25B8E3698A5 CRC64;  
Query Match 14.4%; Score 212.5; DB 1; Length 1070;  
Best Local Similarity 29.1%; Pred. No. 3.6e-09;  
Matches 62; Conservative 34; Mismatches 92; Indels 25; Gaps 7;  
Qy 2 DSPQILVHPDQLFQGGPARMSCRASGPPPTIRLLNGQ-PLSMVPPDPH---HLL 56  
Db 222 ESPARVVLAPQDVVVAAYEEAMFHCQFSQAQPPSLQWLFEDETITNRSRPHLRATVF 281  
Qy 57 PDGTLILLQPPARGHAGHDQALSTDLGVYTCASNRLGTAVSRGARSVAVLREDFQIQP 116  
Db 282 ANGSLLLTVRPR-----NAGIYRCIGQGQRPPILEATLHLAIEDMPLEP 330  
Qy 117 RDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLQPGHRTVYGGSLMARAEKSDX 176  
Db 331 R--VFTAGSERVTCLPKGLPEPSV-WWEHAGVRLPTHGRVYQKGHVLANIAESDAG 387  
Qy 177 TYMCVATNSAGHRES-----RAARVS--IQSPQD 203  
Db 388 VYTCHAANLAGQRQRRQDVNITVATVFSWLKKPQD 420  
RESULT 12

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FT CONFLICT 168 168 /FTid=VSP 002593.
SQ SEQUENCE 1461 AA; 159958 MW; 7AAE897E69635A21 CRC64;
Query Match 14.5%; Score 214.5; DB 1; Length 1461;
Best Local Similarity 22.7%; Pred. No. 3.6e-09;
Matches 79; Conservative 39; Mismatches 117; Indels 113; Gaps 9;
Qy 3 SPQQLVHPQDLOFGPGPARMSCASQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 62
Db 51 TFFVLEVPVDTLSVRGSSVILNAYSSEPKIEWKKGDTFLNLSDDRRQLPDGSLF 110
Qy 63 LLQPPARGHAGDQALSDGLVYTCAS-NRLGTAVSRGRLSVA----- 106
Db 111 ISNVVSHKN-----KDEGYQCVAVESLGTIIISRTAKLIVAGLPRFTSQEPSSVY 164
Qy 107 -----VLRED----- 111
Db 165 AGGAILNCEVNAIDLVPVRWEQNRQPLLLDDRVIKLPSCMLVVISNATEGDGLYRCVVE 224
Qy 112 -----FOIQPRDMVAVVGEQFTLECGPPGHPPTVSWW 145
Db 225 SGGPKYSDEVELKVLDPDEVIDLVFLKQPSPLRVIGQDVLPFCVAS-GLPTTIKWM 283
Qy 146 KDGKPLALQPGRHV--SGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSTQEPQD 203
Db 284 KNEEALDTSESSERVLVLAGGSLEISDVTEDDAGTYFCIADNGNETIEAQAELTVQAQEP 343
Qy 204 YTEPVELLAVRIQLENTVLLNPDPAAGPKPRPAVWLKWKVSGPRKLPN 251
Db 344 LKQPTNIYA----HESMDIVFECEVTG-KPTPTV--KWKVNGDMVIPS 384
RESULT 10
AXOI CHICK STANDARD; PRT; 1036 AA.
AC P28685;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Contactin 2 precursor (Axonin-1).
GN CNTN2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Brain;
RA MEDLINE=9217498; PubMed=1311675;
RA Zuelig R.A., Rader C., Schroeder A., Kalousek M.B.,
RA von Bohlen Und Halbach F., Osterwalder T., Inan C., Stoeckli E.T.,
RA Affolter H.-U., Fritz A., Hafen E., Sonderegger P.;
RT "The axonally secreted cell adhesion molecule, axonin-1. Primary
RT structure, immunoglobulin-like and fibronectin-type-III-like domains
RT and glycosyl-phosphatidylinositol anchorage.";
RL Eur. J. Biochem. 204:453-463(1992).
CC -!- FUNCTION: AXON-ASSOCIATED CELL ADHESION MOLECULE (AXCAM) WHICH
CC PROMOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM L1 (G4)
CC OF NEURITIC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
CC GPI-ANCHOR.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X63101; CAA44815.1; -.
CC PIR; S22383; S22383.
CC PDB; 1CS6; 19-MAY-00.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00041; fn3; 3.
CC Pfam; PF00047; Ig; 6.
CC SMART; SM00408; IGG2; 5.
CC PROSITE; PS00835; IG_LIKE; 6.
KW Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
KW Cell adhesion; Repeat; 3D-structure.
FT SIGNAL 1 23 OR 25 (POTENTIAL)..
FT CHAIN 24 ? CONTACTIN 2.
FT PROPEP ? 1036 REMOVED IN MATURE FORM.
FT DOMAIN 32 123 IG-LIKE C2-TYPE 1.
FT DOMAIN 128 223 IG-LIKE C2-TYPE 2.
FT DOMAIN 234 317 IG-LIKE C2-TYPE 3.
FT DOMAIN 322 406 IG-LIKE C2-TYPE 4.
FT DOMAIN 412 499 IG-LIKE C2-TYPE 5.
FT DOMAIN 504 598 IG-LIKE C2-TYPE 6.
FT DOMAIN 599 608 HINGE (POTENTIAL).
FT DOMAIN 601 607 GLY/PRO-RICH.
FT DOMAIN 608 709 FIBRONECTIN TYPE-III 1.
FT DOMAIN 710 811 FIBRONECTIN TYPE-III 2.
FT DOMAIN 812 912 FIBRONECTIN TYPE-III 3.
FT DOMAIN 913 1009 FIBRONECTIN TYPE-III 4.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 472 472 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 520 520 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 770 770 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 900 900 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1036 AA; 113301 MW; 08B80143BE79794 CRC64;
Query Match 14.5%; Score 213.5; DB 1; Length 1036;
Best Local Similarity 30.7%; Pred. No. 2.9e-09;
Matches 70; Conservative 31; Mismatches 86; Indels 41; Gaps 11;
Qy 24 MSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAGDQALSD 83
Db 54 LTCSRANPPATYRWKNGTELKM-GPDSRYRLVAGDLVISNP-----VKAKDAG 102
Qy 84 VYTCEASNRLGTAVSRGRLSVAVLREDFOIQPRDMVAVV--GEQFTLECGPPGHPPEP 140
Db 103 SYQCVATNARTGVVSRASURFGFLQF-FSAEERDPVKITEGVMWFT--CSPPPHYPAL 159
Qy 141 TVSWKDKGKPLAL-QPGRHVTYS--GGSLLMARAEKSDXTYMCVATNSAGHRE----- 190
Db 160 SYRWLLNEFFNFIPADGRFVSQTTGNLYIAKTEASDLGNYSCEFATS---HIDFTTKSVF 216
Qy 191 SRAARVSI--QEPDYTEPVE-----LLAVRIQLENTVLLNPD 227
Db 217 SKFSQLSLAAEDARQYAPSIKAFKFPADTYALTQMTLECFAGNPVP 264
RESULT 11
PTK7 HUMAN
ID PTK7 HUMAN STANDARD; PRT; 1070 AA.
AC Q13308; Q13417;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase-4)
DE (CCK-4).
GN PTK7 OR CCK4.
```











CC IsoId=P23468-1; Sequence=Displayed;  
 CC Name=2; Synonym=Kidney;  
 CC IsoId=P23468-2; Sequence=VSP\_005147, VSP\_005148, VSP\_005149;  
 CC Name=3; Synonym=Fetal brain;  
 CC IsoId=P23468-3; Sequence=VSP\_005150;  
 CC FROM THE TRANSMEMBRANE SEGMENT.  
 CC -1- CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN  
 CC FROM THE TRANSMEMBRANE SEGMENT.  
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
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 CC -----  
 CC EMBL; L38929; AAC41749.1; -;  
 CC EMBL; X54133; CAA38068.1; -;  
 CC PIR; A56178; A56178.  
 CC HSSP; P18052; 1YFO.  
 CC Genew; HGNC:9668; PTPRD.  
 CC MIM; 601598; -;  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005001; P:transmembrane receptor protein tyrosine pho. . .; TAS.  
 CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 CC GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.  
 CC InterPro; IPR003961; FN\_III.  
 CC InterPro; IPR003962; FNIII\_subd.  
 CC InterPro; IPR007110; IG-like.  
 CC InterPro; IPR003598; IG\_c2.  
 CC InterPro; IPR003006; IG\_MHC.  
 CC InterPro; IPR000387; TYR phosphatase.  
 CC InterPro; IPR000242; Tyr\_PP.  
 CC Pfam; PF00041; fn3; 8.  
 CC Pfam; PF00047; ig; 3.  
 CC Pfam; PF00102; Y\_phosphatase; 2.  
 CC PRINTS; PR00014; FNTYPEIII.  
 CC PRINTS; PR00700; PRTPHPTASE.  
 CC SMART; SM00060; FN3; 8.  
 CC SMART; SM00408; IGC2; 2.  
 CC SMART; SM00194; PTPC; 2.  
 CC PROSITE; PS00835; IG LIKE; 3.  
 CC PROSITE; PS00383; TYR PHOSPHATASE 1; 2.  
 CC PROSITE; PS00056; TYR PHOSPHATASE 2; 2.  
 CC PROSITE; PS00055; TYR PHOSPHATASE\_PTP; 2.  
 CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;  
 CC Immunoglobulin domain; Alternative splicing.  
 CC SIGNAL 1 20  
 CC CHAIN 21 1912  
 CC DOMAIN 21 1265  
 CC TRANSMEM 1266 1290  
 CC DOMAIN 1291 1912  
 CC DOMAIN 24 114  
 CC DOMAIN 126 224  
 CC DOMAIN 236 318  
 CC DOMAIN 320 414  
 CC DOMAIN 417 513  
 CC DOMAIN 516 606  
 CC DOMAIN 609 708  
 CC DOMAIN 711 822  
 CC DOMAIN 825 916  
 CC DOMAIN 918 1017  
 CC DOMAIN 1020 1137  
 CC DOMAIN 1375 1618  
 CC DOMAIN 1619 1912  
 CC ACT\_SITE 1553 1553  
 CC ACT\_SITE 1844 1844  
 CC SITE 1175 1178  
 CC CARBOHYD 254 254  
 CC CARBOHYD 299 299

FT CARBOHYD 724 724 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 832 832 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 181 189 Missing (in isoform 2).  
 FT VARSPLIC 226 229 Missing (in isoform 2).  
 FT VARSPLIC 775 783 Missing (in isoform 2).  
 FT VARSPLIC 609 1137 Missing (in isoform 3).  
 FT MUTAGEN 1178 1178 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.  
 SQ SEQUENCE 1912 AA; 214759 MW; 3A88CBDC32182E26 CRC64;  
 Query Match 15.1%; Score 222; DB 1; Length 1912;  
 Best Local Similarity 32.5%; Pred. No. 1.3e-09;  
 Matches 74; Conservative 37; Mismatches 67; Indels 50; Gaps 14;  
 QY 2 DSPQILVHPQDLFOGPGPARMSCRAGQPPPTIRWLLNGQPLS-----MVPDPHLL 56  
 DB 21 ETPPRFTRTPVDQTGVSGVASFCQATGDPRPKIVVWKKGVSNORFEVIEFDD---- 76  
 QY 57 PDGTLTLLQPPARGHAGHGGALST--DLGVYTCASNRLGTAVSRGARLSVAVLRDPQI 114  
 DB 77 GSGSVLRIQP-----LRTPRDEAIYECVASNNVG-EISVSTRLT--VLRED-QI 121  
 QY 115 QPRDMVAV-VGEQF-----TLECGPPWGHPEPTVSWMKGKPL--ALQPCR----- 157  
 DB 122 -PRGFPIDMGPKLVKVERTRTATMLCAAS-GNPDPEITWFKDLPLVDTSNNNGRIKQLR 179  
 QY 158 -HTVSG-----GSLMARAEKSDXTYMCVATNSAGHRESRAARVSIQE 200  
 DB 180 SESGGTPIRGALQIEQSESDQGYECVATNSAGTRYSPANLYVRE 227  
 RESULT 6  
 LAR\_DROME  
 ID LAR DROME STANDARD; PRT; 2029 AA.  
 AC P16621;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Protein-tyrosine phosphatase lar precursor (EC 3.1.3.48) (Protein-  
 DE tyrosine-phosphate phosphohydrolase) (dLAR).  
 GN LAR.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90046860; PubMed=2554325;  
 RT Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 and Drosophila";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Canton-S;  
 RX MEDLINE=96178473; PubMed=8598047;  
 RA Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,  
 RA Saito H.;  
 RT "The transmembrane tyrosine phosphatase DLAR controls motor axon  
 RT guidance in Drosophila";  
 RL Cell 84:611-622(1996).  
 CC -1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.  
 CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY  
 CC (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND  
 CC PIONEER NEURONS IN THE EMBRYO.

FT	DOMAIN	924	933	LAMININ EGF-LIKE 5 (N-TERMINAL).	FT	DISULFID	1641	1650	BY SIMILARITY.
FT	DOMAIN	934	1125	LAMININ DOMAIN IV 2 (DOMAIN III B).	FT	DISULFID	1653	1668	BY SIMILARITY.
FT	DOMAIN	1126	1158	LAMININ EGF-LIKE 5 (C-TERMINAL).	FT	DISULFID	1792	1839	BY SIMILARITY.
FT	DOMAIN	1159	1208	LAMININ EGF-LIKE 6.	FT	DISULFID	1886	1932	BY SIMILARITY.
FT	DOMAIN	1209	1285	LAMININ EGF-LIKE 7.	FT	DISULFID	1976	2021	BY SIMILARITY.
FT	DOMAIN	1275	1324	LAMININ EGF-LIKE 8.	FT	DISULFID	2073	2118	BY SIMILARITY.
FT	DOMAIN	1325	1334	LAMININ EGF-LIKE 9 (N-TERMINAL).	FT	DISULFID	2170	2215	BY SIMILARITY.
FT	DOMAIN	1335	1529	LAMININ DOMAIN IV 3 (DOMAIN III C).	FT	DISULFID	2268	2313	BY SIMILARITY.
FT	DOMAIN	1530	1562	LAMININ EGF-LIKE 9 (C-TERMINAL).	FT	DISULFID	2365	2413	BY SIMILARITY.
FT	DOMAIN	1563	1612	LAMININ EGF-LIKE 10.	Query Match 15.3%; Score 225; DB 1; Length 3707;				
FT	DOMAIN	1613	1670	LAMININ EGF-LIKE 11.	Best Local Similarity 27.6%; Pred. No. 1.6e-09;				
FT	DOMAIN	1677	1771	IG-LIKE C2-TYPE 2.	Matches 72; Conservative 37; Mismatches 86; Indels 66; Gaps 13;				
FT	DOMAIN	1772	1865	IG-LIKE C2-TYPE 3.	QY 4 PQQLVHPQDQLFOGPGPARM-----SCRASGPPPTIRWLLNGQPLSMWP-----PDP 52				
FT	DOMAIN	1866	1954	IG-LIKE C2-TYPE 4.	DB 2433 PPTVSVLP-----EGPVHVRMGKDIITLCISSGEPRSPRWTRLGIPVKLEPRMGLMNS 2487				
FT	DOMAIN	1955	2049	IG-LIKE C2-TYPE 5.	QY 53 HLLLPDGTLLLPARGHAGHDGQALSTDLGVYTCESNRILGTA-----VSRGARLSV 105				
FT	DOMAIN	2050	2148	IG-LIKE C2-TYPE 6.	DB 2488 HAML---KIASVKP-----SDATYVCOAQNALGTAQKQVELIVDTG---TV 2528				
FT	DOMAIN	2149	2244	IG-LIKE C2-TYPE 7.	QY 106 AVLREDFQIOPRDMVAVVGEQFTLECGPFPGHPPTVSWKDGKPLALQPGRHVTVSGSL 165				
FT	DOMAIN	2245	2343	IG-LIKE C2-TYPE 8.	DB 2529 APGTPQVQVESELTLGAGHTATLHCSAT-GNPPPTIHWKLRAPL---PWQHRIEGNTL 2584				
FT	DOMAIN	2344	2436	IG-LIKE C2-TYPE 9.	QY 166 LMAAEKSDXTYMCVATNSAGHRESRAARVISIEPQDYT-----EPVELLAVRIQL 217				
FT	DOMAIN	2437	2532	IG-LIKE C2-TYPE 10.	DB 2585 VIPRAQODSQYICNATNSAGHTEATVV-LHVESPPYATIPEHTSAQGNL-----VOL 2639				
FT	DOMAIN	2533	2619	IG-LIKE C2-TYPE 11.	QY 218 ENVTLLNPDPAGEPKPRPAVW 238				
FT	DOMAIN	2620	2720	IG-LIKE C2-TYPE 12.	DB 2640 QCL-----ANGTPPLTYQW 2653				
FT	DOMAIN	2721	2809	IG-LIKE C2-TYPE 13.	RESULT 5				
FT	DOMAIN	2810	2895	IG-LIKE C2-TYPE 14.	PTPD HUMAN				
FT	DOMAIN	2896	2980	IG-LIKE C2-TYPE 15.	ID_PTPD HUMAN STANDARD; PRT; 1912 AA.				
FT	DOMAIN	2984	3162	LAMININ G-LIKE 1.	AC P23468;				
FT	DOMAIN	3163	3241	EGF-LIKE.	DT 01-NOV-1991 (Rel. 20, Created)				
FT	DOMAIN	3245	3425	LAMININ G-LIKE 2.	DT 01-OCT-1996 (Rel. 34, Last sequence update)				
FT	DOMAIN	3518	3705	HEPARAN SULFATE (POTENTIAL).	DT 15-SEP-2003 (Rel. 42, Last annotation update)				
FT	SITE	65	67	HEPARAN SULFATE (POTENTIAL).	DE protein-tyrosine phosphatase delta precursor (BC 3.1.3.48) (R-PTP-				
FT	SITE	71	73	HEPARAN SULFATE (POTENTIAL).	GN PTPRD.				
FT	SITE	76	78	MEDIATES MOTOR NEURON ATTACHMENT	OS Homo sapiens (Human).				
FT	SITE	3615	3617	(POTENTIAL).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
FT	DISULFID	199	212	BY SIMILARITY.	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
FT	DISULFID	206	225	BY SIMILARITY.	OX NCBI_TaxID=9606;				
FT	DISULFID	219	234	BY SIMILARITY.	RN [1]				
FT	DISULFID	285	297	BY SIMILARITY.	RX SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.				
FT	DISULFID	222	310	BY SIMILARITY.	RX MEDLINE=9520468; PubMed=7896816;				
FT	DISULFID	304	319	BY SIMILARITY.	RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;				
FT	DISULFID	325	337	BY SIMILARITY.	RT "Molecular characterization of the human transmembrane protein-				
FT	DISULFID	332	350	BY SIMILARITY.	RT tyrosine phosphatase delta. Evidence for tissue-specific expression of				
FT	DISULFID	344	359	BY SIMILARITY.	RT alternative human transmembrane protein-tyrosine phosphatase delta				
FT	DISULFID	368	381	BY SIMILARITY.	RT isoforms.";				
FT	DISULFID	375	394	BY SIMILARITY.	RL J. Biol. Chem. 270:6722-6728 (1995).				
FT	DISULFID	388	403	BY SIMILARITY.	RN [2]				
FT	DISULFID	428	479	BY SIMILARITY.	RC TISSUE=Placenta;				
FT	DISULFID	764	773	BY SIMILARITY.	RX MEDLINE=91006018; PubMed=2170109;				
FT	DISULFID	766	780	BY SIMILARITY.	RA Krueger N.X., Streuli M., Saito H.;				
FT	DISULFID	783	792	BY SIMILARITY.	RT "Structural diversity and evolution of human receptor-like protein				
FT	DISULFID	795	811	BY SIMILARITY.	RT tyrosine phosphatases.";				
FT	DISULFID	814	829	BY SIMILARITY.	RL EMBO J. 9:3241-3252 (1990).				
FT	DISULFID	816	839	BY SIMILARITY.	CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein				
FT	DISULFID	842	851	BY SIMILARITY.	CC Tyrosine + phosphate.				
FT	DISULFID	854	869	BY SIMILARITY.	CC -I- SUBCELLULAR LOCATION: Type I membrane protein.				
FT	DISULFID	1159	1168	BY SIMILARITY.	CC -I- ALTERNATIVE PRODUCTS:				
FT	DISULFID	1161	1175	BY SIMILARITY.	CC Event=Alternative splicing; Named isoforms=3;				
FT	DISULFID	1178	1187	BY SIMILARITY.	CC Comment=Additional isoforms seem to exist;				
FT	DISULFID	1209	1224	BY SIMILARITY.	CC Name=1;				
FT	DISULFID	1211	1234	BY SIMILARITY.					
FT	DISULFID	1237	1246	BY SIMILARITY.					
FT	DISULFID	1249	1263	BY SIMILARITY.					
FT	DISULFID	1275	1287	BY SIMILARITY.					
FT	DISULFID	1277	1293	BY SIMILARITY.					
FT	DISULFID	1295	1304	BY SIMILARITY.					
FT	DISULFID	1307	1322	BY SIMILARITY.					
FT	DISULFID	1307	1322	BY SIMILARITY.					
FT	DISULFID	1563	1572	BY SIMILARITY.					
FT	DISULFID	1565	1579	BY SIMILARITY.					
FT	DISULFID	1582	1591	BY SIMILARITY.					
FT	DISULFID	1594	1610	BY SIMILARITY.					
FT	DISULFID	1613	1628	BY SIMILARITY.					
FT	DISULFID	1615	1638	BY SIMILARITY.					

;; PRIOR APPLICATION NUMBER: 60/081838  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/082568  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082569  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082704  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082804  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082700  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082796  
;; PRIOR FILING DATE: 1998-04-23  
;; PRIOR APPLICATION NUMBER: 60/083336  
;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-30  
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;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084600  
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;; PRIOR APPLICATION NUMBER: 60/084627  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085339  
;; PRIOR FILING DATE: 1998-05-13  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Kijavini, Ivar J.  
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; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Shelton, David L.  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC9  
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US-10-047-021-86 (1-303) x US-09-978-192A-210 (1-3716)

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman







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Mismatches:	3
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Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGCATGGCTCAGACTCCCGCCAGATCTCTAGTCCACCCCGCCAGCAGCTGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db 121 CAGGCCCTGGCCCTGGCAGATGAGCTGCGAGGCTCAGGCTCAGCCAGCCATC 180
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeu 83
Db 181 CGCTGGTTGCTGAATGGGAGCCCTGAGCATGGTGGCCCGCCAGACCCACCTCT 240
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Db 241 CCTGATGGAGCCCTTCTGCTGCTACAGCCCTGCGCCGGGACATGCGCCAGT 300
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerHisArgLeuThrAla 123
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Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgLeuSerPheGlnPro 143
Db 361 GTCAGCAGAGCGCTCGGCTGCTGTGGCTGTCTCGGGGAGGATTTCCAGATCC 420
Qy 144 ArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163
Db 421 CGGACATGGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG 480
Qy 164 HisProGluProThrValSerTrpTrpAspGlyLysProLeuAlaLeuGlnProGly 183
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Qy 204 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaArgVal 223
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Qy 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProC 283
Db 781 GTGTGGCTCAGCTGGAAGGTGAGTGGCCCTCTGTCGCTGCGCCATCTTACAC 840
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGGCCAGACTGCCCCGGAGGCCAGGAGCTCGGTGGGAGAGG 889
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; Sequence 210, Application US/0978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Pred. No.: 1550.00 Matches: 292
Score: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 11 Gaps: 0
US-10-047-021-86 (1-303) x US-09-978-585A-210 (1-3716)
Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGAGACAGCTCTCTGGGGGAGGGTTCCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGCATGGCTCAGGACTCCCGCCAGATCTCTAGTCCACCCCGCCAGCAGCTGTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63
Db 121 CAGGCCCTGGCCCTGGCAGATGAGCTGCGAGGCTCAGGCTCAGCCAGCCATC 180
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeu 83
Db 181 CGCTGGTTGCTGAATGGGAGCCCTGAGCATGGTGGCCCGCCAGACCCACCTCT 240
Qy 84 ProAspGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuGln 103
Db 241 CCTGATGGAGCCCTTCTGCTGCTACAGCCCTGCGCCGGGACATGCGCCAGT 300
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerHisArgLeuThrAla 123
Db 301 GCCCTGTCCACAGACCTGGGGTGTCTACATGTGAGGCCAGCAACCGGCTTGG 360
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgLeuSerPheGlnPro 143
Db 361 GTCAGCAGAGCGCTCGGCTGCTGTGGCTGTCTCGGGGAGGATTTCCAGATCC 420
Qy 144 ArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163
Db 421 CGGACATGGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG 480
Qy 164 HisProGluProThrValSerTrpTrpAspGlyLysProLeuAlaLeuGlnProGly 183
Db 481 CACCAGAGCCACAGTCTCATGGTGAAGATGGAAACCCCTGGCCCTCCAGCCGG 540
Qy 184 ArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
Db 541 AGGCACACAGTGTCCGGGGGCTCTCTGCTGATGCAAGAGCAGAGAGTGCAGAG 600
Qy 204 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaArgVal 223
Db 601 ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCGG 660
Qy 224 SerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaValArgIleGln 243
Db 661 TCCATCCAGGAGCCCGAGACTACACGAGGCTGTGGAGCTTCTGGCTGCGAATT 720
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263
Db 721 CTGGAATAATGTGACACTCTGAACCCGATCTCTGAGAGGCGCCCAAGCCGAG 780
Qy 264 ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProC 283
Db 781 GTGTGGCTCAGCTGGAAGGTGAGTGGCCCTCTGTCGCTGCGCCATCTTACAC 840
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
Db 841 TTCAGGCCAGACTGCCCCGGAGGCCAGGAGCTCGGTGGGAGAGG 889
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 ; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
 Pred. No.: 2,9e-136 Length: 3716  
 Score: 1550.00 Matches: 292  
 Percent Similarity: 98.65% Conservative: 1  
 Best Local Similarity: 98.32% Mismatches: 3  
 Query Match: 96.39% Indels: 1  
 DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-191A-210 (1-3716)

Qy	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet	23
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Qy	24	GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe	43
Db	61	GGAGGCATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACCATG	120
Qy	44	GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle	63
Db	121	CAGGGCCCTGGCCCTGCCAGGATGAGCTGCGCAAGCCTCAGGCAGCCACCTCCACC	180
Qy	64	ArgTrpLeuLeuGlnProLeuSerMetValProProAspProHisHisLeuLeu	83
Db	181	CGCTGGTTGCTGAATGGGCGAGCCCTGAGCATGTGTGTCGCCAGACCCACACCTCTG	240
Qy	84	ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln	103
Db	241	CCTGATGGGACCCCTTCTGCTGTCTACAGCCCTGCCCGGGGACATGCCCAGATGGCCAG	300
Qy	104	AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAla	123
Db	301	GCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTTGGCAGCGCA	360
Qy	124	ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro	143
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Qy	184	ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu***	203
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QY 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
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; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
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; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C17  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:

2.9e-136

Length:

3716

Score: 1550.00 Matches: 292  
Percent Similarity: 98.65% Conservative: 1  
Best Local Similarity: 98.32% Mismatches: 3  
Query Match: 96.39% Indels: 1  
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-403A-210 (1-3716)

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Qy 24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43  
Db 61 GGAGGCATGGCTCAGGACTCCCGCCCCCAGATCCTAGTCCACCCAGGACCACTGTTTC 120  
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63  
Db 121 CAGGGCCCTGGCCCTGCGAGGATGAGCTGCAAGCCTCAGGCCAGCACTCCCAACCATC 180  
Qy 64 ArgTrpLeuLeuGlnProLeuSerMetValProProAspProHisLeuLeu 83  
Db 181 CGCTGGTTGCTGAATGGGCAGCCCTGAGCATGGTGTCCCGCAGACCCACACCTCTCTG 240  
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103  
Db 241 CCTGATGGGACCCCTTCTGCTGTCTACAGCCCTCCCGGGGACATGCCAGATGGCCAG 300  
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGlnAlaSerAsnArgLeuGlyThrAla 123  
Db 301 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCA 360  
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143  
Db 361 GTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCCGGAGGATTTCCAGATCCAGCCT 420  
Qy 144 ArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163  
Db 421 CGGGACATGTGGCTGTGGTGGTGAGCAGTTTACTCTGGAAATGTGGCCCGCCCTGGGGC 480  
Qy 164 HisProGlnProThrValSerTrpTrpLeuAspGlyLysProLeuAlaLeuGlnProGly 183  
Db 481 CACCCAGAGCCACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA 540  
Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\* 203  
Db 541 AGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTGACGAAGG 600  
Qy 204 ThrTrpMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAArgVal 223  
Db 601 ACCTACATGTGTGGCCACACAGCGCAGGACATAGGGAGAGCCCGCGCAGCCGGGTT 660  
Qy 224 SerIleGlnProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243  
Db 661 TCCATCCAGGAGCCCGCAGGACTACACGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAG 720  
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263  
Db 721 CTGGAAAATGTGACACTGTGAACCCCGGATCCTGACAGAGGGCCCGCAGACCTAGACCGGCG 780  
Qy 264 ValTrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCys 283  
Db 781 GTGTGGCTCAGCTGGAAGGTTCAGTGGCCCTGCTGCGCTGCCCAATCTTACACGGCCTTG 840  
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
Db 841 TTCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGG 889

RESULT 13

US-09-978-564A-210

; Sequence 210, Application US/09978564A

; Publication No. US20030050241A1

; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC25  
CURRENT APPLICATION NUMBER: US/09/978,564A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2,9e-136 Length: 3716  
Score: 1550.00 Matches: 292  
Percent Similarity: 98.65% Conservative: 1  
Best Local Similarity: 98.32% Mismatches: 3  
Query Match: 96.39% Indels: 1  
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-564A-210 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23  
Db 1 GGAGGAGACGCCCTCTGGGGGAGGGGTTCCCTGCTCTGCTGCTCTCATG 60  
Qy 24 GlyGlyMetAlaGlnAspSerProProGlnLeuValHisProGlnAspGlnLeuPhe 43  
Db 61 GGAGGATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGAGGACCACTGTT 120  
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThre 63  
Db 121 CAGGCCCCCTGGCCCTGCCAGGATGAGTGCACCAAGCCTCAGGCGCACCACTCCCA 180

Qy 64 ArcTripleLeuLeuAasnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 83  
Db 181 CGCTGGTTGCTGAATGGGAGAGCCCTTGAGCATGGTCCCCCAGACCCACACCTCTCTG 240  
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103  
Db 241 CCTGATGGGACCTTCTGCTGTCTACAGCCCTCCCGGGGACATGCCCACGATGGCCAG 300  
Qy 104 AlaLeuSerThrAspLeuGlyValThrCysGlnAlaSerAsnArgLeuGlyThrAla 123  
Db 301 GCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTGGCACGGCA 360  
Qy 124 ValSerArgGlyValAlaArgLeuSerValAlaValLeuArgGluAspPheGlnLeuPro 143  
Db 361 GTGAGCAGAGCGCTCGGCTGTCTGGGTGTCTCGGGAGGATTTCCAGATCCAGCCT 420  
Qy 144 ArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyProProTriPly 163  
Db 421 CGGACATGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 480  
Qy 164 HisProGlnProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183  
Db 481 CACCCAGAGCCACAGTCTCATGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA 540  
Qy 184 ArcHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu 203  
Db 541 AGGCACACAGTGTCCGGGGGTCTCTGCTGTGTGCAAGACAGAGAGAGTGCACCAAGG 600  
Qy 204 ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223  
Db 601 ACCTACATGTGTGGCCCAACACAGCGCAGGACATAGGAGAGCGCGCAGCCGGGTT 660  
Qy 224 SerIleGlnProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln 243  
Db 661 TCCATCCAGGAGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGGTGTGCGAATTCAG 720  
Qy 244 LeuGluAasnValThrLeuLeuAasnProAspProAlaGluGlyProLysProArgProAla 263  
Db 721 CTGGAAATGTGACACTGTGAACCGGATCTGCAAGAGGGCCCCCAGACCTTAGACCCGG 780  
Qy 264 ValTrpLeu\*\*TrpLysValSerGlyPro\*\*\*ArgLeuProAasnLeuThrArgProCy 283  
Db 781 GTGTGGCTCAGTGGAAAGTTCAGTGGCCCTGCTGCGCTGCCCAATCTTACACGGCCTTG 840  
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
Db 841 TTCAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG 889

## RESULT 14

US-09-999-833A-210  
; Sequence 210, Application US/09999833A  
; Publication No. US20030054405A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC65  
CURRENT APPLICATION NUMBER: US/09/999,833A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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Alignment Scores:
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Score:          1550.00      Matches:      292
Percent Similarity: 98.65%      Conservative: 1
Best Local Similarity: 98.32%      Mismatches: 3
Query Match:      96.39%      Indels:      1
DB:              11          Gaps:      0

US-10-047-021-86 (1-303) x US-09-999-833A-210 (1-3716)

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Db 1 GGAGGAGACACCTCTCTGGGGGGGAGGGGTTCCCTGCTGCTGCTGCTGCTGCTCATG 60

Qy 24 GlyGlyMetAlaGlnAspSerProGlnleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGCGATGGCTCAGGACTCCCGCCCGCCAGATCTAGTCCACCCCGCCAGGACCATGTC 120

Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrile 63
Db 121 CAGGCGCCCTGGCCCTGCCAGGATGAGTGTCCCAAGCCTCAGGCGCCACCTCCCAACCATC 180

Qy 64 ArgTrpLeuLeuAenGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83
Db 181 CGCTGGTTGCTGATGGGACCCCTGAGCATGTGTGCCCCAGACCCACACCATCTCTG 240

Qy 84 ProaspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
Db 241 CCTGATGGGACCTTCTGCTCTACAGCCCTGCCCGGGGACATGCCACGATGGCCAG 300

Qy 104 AlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThAla 123
Db 301 GCCCTGTCCACAGACCTGGGGTGTCTACACATGTGAGGCGCAGCAACCGGCTTGGCAGCGCA 360

Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnleGlnPro 143
Db 361 GTACAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTTCCGGAGAGATTTCAGATCCAGCCT 420

Qy 144 ArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163
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## RESULT 15

US-09-981-915A-210

; Sequence 210, Application US/09981915A

; Publication No. US20030054986A1

; GENERAL INFORMATION:

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; APPLICANT: Eaton, Dan

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; APPLICANT: Filvaroff, Ellen

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; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

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; APPLICANT: Grimaldi, J. Christopher

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; APPLICANT: Hillan, Kenneth J.

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; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C12

; CURRENT APPLICATION NUMBER: US/09/981.915A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

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; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03



;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. NO.:	2.9e-136	Length:	3716
Score:	1550.00	Matches:	292
Percent Similarity:	98.65%	Conservative:	1
Best Local Similarity:	98.32%	Mismatches:	3
Query Match:	96.39%	Indels:	1
DB:	11	Gaps:	0

US-10-047-021-86 (1-303) x US-09-981-915A-210 (1-3716)

Qy	4	GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMet	23
Db	1	GGAGGAGACACCTCTCTGGGGGGGAGGGGTTCCCTGCTCTGCTGCTCTCTCATG	60
Qy	24	GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe	43
Db	61	GGAGGCATGGCTCAGGACTCCCGCCCCAGATCTTAGTCCACCCCGGAGGACGAGTTC	120
Qy	44	GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle	63
Db	121	CAGGGCCCTGCCCTGCCAGATGAGTGCAGGCTCCAGGCTCAGGCTCCACCATC	180
Qy	64	ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu	83
Db	181	CGTGGTTGCTGAATGGGACCCCTGAGCATGGTGGCCCCGAGCCACACCATCTCTG	240
Qy	84	ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln	103
Db	241	CCTGATGGGACCTTCTCTCTCAGCCCTGCTGGGGGACATGCCACGATGGCCAG	300
Qy	104	AlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeuGlyThrAla	123
Db	301	GCCTGTCCAGACCTGGGTGTCTACACATGTGAGGCGAGCAACCGGCTTGGCAGGCA	360
Qy	124	ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro	143
Db	361	GTCAGCAGGCGCTCGGCTGTCTGTGGCTGTCTCCGGAGGATTTCCAGATCCAGCCT	420
Qy	144	ArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyProProTrpGly	163
Db	421	CGGGACATGGTGGCTGTGGTGGGAGCAGTTTACTCTGGAATGTGGGCCCGCTGGGGC	480
Qy	164	HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly	183
Db	481	CACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGGCCCTCCAGCCCGGA	540
Qy	184	ArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu**	203
Db	541	AGGCACACAGTGTCCGGGGGGTCCCTGCTGTATGGCAGAGCAGAGAGTGCAGAGGG	600
Qy	204	ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal	223
Db	601	ACCTACATGTGTGTGGCCACCAAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGTT	660
Qy	224	SerIleGlnGluProGlnAspTyThrGlnProValGluLeuLeuAlaValArgIleGln	243
Db	661	TCCATCCAGGAGCCCCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTGCGAATTCAG	720
Qy	244	LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla	263

Db	721	CTGGAAATGTGACACTGCTGAACCCGATCTCTGAGAGGGGCCCAAGCCTAGACCGCG	780
Qy	264	ValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThrArgProCy	283
Db	781	GTGTGGCTCAGCTGGAGGTCAGTGGCCCTGCTGCGCTGCCCAATCTTACACGCGCTTG	840
Qy	283	sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg	299
Db	841	TTACAGGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGGCAGAGG	889

Search completed: January 31, 2004, 17:18:16  
Job time : 345.352 secs



Result No.	Score	Query Match	Length	DB	ID	Description
1	448.5	27.9	1651	2	T14160	transmembrane rece
2	445.5	27.7	1612	2	T30805	dutt1 protein - mo
3	414.5	25.8	1344	2	T14316	rig-1 protein - mo
4	360	22.4	1273	2	T42405	sax-3 protein - Ca
5	356.5	22.2	423	2	T29549	hypothetical prote
6	253.5	15.8	1898	2	S46216	leukocyte antigen-
7	253	15.7	1535	2	S46224	peroxidase - frui
8	251	15.6	1272	2	S26180	neurofascin - chic
9	245	15.2	1497	2	I51669	tumor suppressor -
10	244.5	15.2	1897	1	TDHULK	leukocyte antigen-
11	237.5	14.8	1501	2	I58148	protein-tyrosine-p
12	237.5	14.8	1863	2	S46217	protein-tyrosine-p
13	237.5	14.8	1907	2	S50893	protein-tyrosine-p
14	236.5	14.7	1040	2	A34695	axonal glycoprotei
15	232	14.4	1040	2	A49356	transient axonal g
16	231.5	14.4	3707	2	I8252	heparan sulfate pr
17	230	14.3	1912	2	A56178	protein-tyrosine-p
18	228	14.2	1028	2	A53449	plasmacytoma- assoc
19	228	14.2	1894	2	C54689	protein-tyrosine-p
20	228	14.2	5175	2	T20992	hypothetical prote
21	228	14.2	5198	2	T43290	hemikentil precurs
22	227.5	14.1	1028	2	I58164	BIG-1 protein - ra
23	227.5	14.1	1262	1	B48758	protein-tyrosine-p
24	227.5	14.1	1496	1	A48758	protein-tyrosine-p
25	222	13.8	2029	1	TDPELK	protein-tyrosine-p
26	220.5	13.7	1499	2	I50212	protein-tyrosine-p
27	217.5	13.5	1070	2	JC4593	protein-tyrosine k
28	216	13.4	1239	1	A32579	neuroglian - frui
29	215.5	13.4	1443	2	I50600	neogenin - chicken



Db 25 ASNLAPVIEHPIDVVRSGSPATLNC---GAKPSTAKITVKGOPVITNKEQVNSHRI 81  
QY 83 LPD-GTLLQLPPARGHAGDQALSTDLGVYTCASNRRLGTAVSRGARLSVAVLRFQI 141  
Db 82 VLDTGSFLFKVNSGKNGD-----SDAGAYCVASNEHGEVKSNEGSLKLAWLREDFRV 136  
QY 142 QPRDMVAVGEOFTLECGPPHGPPTVSWKDGKPLALQ-GRHTV-SGGSLLMARAEK 199  
Db 137 RPRVTQALGGENAVLECSPPRGFPFVSVWRKDKELARIQDMPRVTLTSDGNLIIDPVD 196  
QY 200 SDEXTYMCVATNSAGHRSRAARVSI-----QSPQDYTEPVELLAVRIQLENTLNP 252  
Db 197 SDSGTYQQCVANMVGERVSNPARLSVFEKPEQPKDMT-----VDGAALVDFC 247  
QY 253 DPAEGPKPRPAVWLKVKVSGPRLNLTPLPCGPRLPREARELRQR 299  
Db 248 RVTGDPQPO-----ITWK-----RKNEPMVTVTRAIANDNRGLRIER 284

RESULT 6  
S46216  
N:leukocyte antigen-related protein precursor - rat  
N:Alternate names: leukocyte common antigen homolog  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S46216; S23252; A41032; A33154  
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
Biochem. J. 302, 39-47, 1994  
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase from rat  
A:Reference number: S46216; MUID:94347119; PMID:8068021  
A:Accession: S46216  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1898 <ZHA>  
A:CROSS-references: EMBL:L11586; NID:G205132; PIDN:AAC37655.1; PID:G205133  
R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
Biochem. J. 284, 569-576, 1992  
A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three different tyrosine phosphatases  
A:Reference number: S23126; MUID:92287069; PMID:1599438  
A:Accession: S23252  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1361-1604/1649-1898 <HAS>  
R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
J. Biol. Chem. 266, 19688-19696, 1991  
A:Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic domain of the insulin receptor  
A:Reference number: A41032; MUID:92011772; PMID:1918076  
A:Accession: A41032  
A:Molecule type: mRNA  
A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
A:CROSS-references: GB:M60103; NID:G205130; PIDN:AAA41510.1; PID:G205131  
R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
submitted to the Protein Sequence Database, December 1990  
A:Reference number: A33154  
A:Accession: A33154  
A:Molecule type: mRNA  
A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
C:Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogy

C:Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; C  
F:1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>  
F:28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT  
F:28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>  
F:47-109/Domain: immunoglobulin homology <IMM1>  
F:149-209/Domain: immunoglobulin homology <IMM2>  
F:246-300/Domain: immunoglobulin homology <IMM3>  
F:318-400/Domain: fibronectin type III repeat homology <FN3A>  
F:413-499/Domain: fibronectin type III repeat homology <FN3B>  
F:511-593/Domain: fibronectin type III repeat homology <FN3C>  
F:606-695/Domain: fibronectin type III repeat homology <FN3D>  
F:708-799/Domain: fibronectin type III repeat homology <FN3E>

F:811-895/Domain: fibronectin type III repeat homology <FN3F>  
F:906-990/Domain: fibronectin type III repeat homology <FN3G>  
F:1002-1079/Domain: fibronectin type III repeat homology <FN3H>  
F:1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TMM>  
F:1276-1898/Domain: intracellular #status predicted <INT>  
F:1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:54-107, 156-207, 253-298/Disulfide bonds: #status predicted  
F:117, 250, 295, 721, 957/Binding site: carbohydrate (Aen) (covalent) #status predicted  
F:1539/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1539/Binding site: substrate phosphate (Arg) #status predicted  
F:1830/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1836/Binding site: substrate phosphate (Arg) #status predicted

Query Match 15.8%; Score 253.5; DB 2; Length 1898;  
Best Local Similarity 31.8%; Pred. No. 9.3e-11;  
Matches 75; Conservative 41; Mismatches 83; Indels 37; Gaps 10;

QY 11 GRGSLP-----LLLLLIMGMAQDPPQILVHPDQLFQGPGRMCRSCASGQPPPTIRWL 66  
Db 8 GRMVPLVPLVLMGLMAGAGHDSKPVFVKVPEDQIGLGGVASFVCQATGEPKPRITWM 67  
QY 67 LNCQPLS-----MVPDPHLLPDGTLTLLLPARGHAGDQALSTDLGVYTCASNRRL 121  
Db 68 KKGKKVSSQRFEVIEFDD---GAGSVLRIQP-----LRVQDEAIYECTATNSLG 114  
QY 122 TAVSRGARLSVAVLRED-----FQIQPRDMVAVGEEQFTLECGPPHGPPTVSWK 173  
Db 115 -EIMTSAKLS--VLEEDQLPSGFTIDMGPKVVEKARTATMLCA-AGNPDPBISWFK 170  
QY 174 DGKPL--ALQGR-HTVSGSLLMARAEKSDXTVMCVATNSAGHRSRAARVSIQ 226  
Db 171 DFLPVDPASSNGRIKQLRSGLAQIESSESDQKVECVATNSAGTRYAPANLYR 226

RESULT 7  
S46224  
peroxidase - fruit fly (Drosophila sp.)  
C:Species: Drosophila sp.  
C:Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text\_change 24-Oct-2000  
C:Accession: S46224  
R:Nelson, R.E.; Feesler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; Parke  
EMBO J. 13, 3438-3447, 1994  
A:Title: Peroxidase: a novel enzyme-matrix protein of Drosophila development.  
A:Reference number: S46224; MUID:94341255; PMID:8062820  
A:Accession: S46224  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1535 <NEL>  
A:CROSS-references: GB:U11052; NID:G531384; PIDN:AAA61568.1; PID:G531385  
C:Superfamily: peroxidase; myeloperoxidase homology; proteoglycan amino-terminal homology  
F:19-44/Domain: proteoglycan amino-terminal homology <PAH4>  
F:661-1350/Domain: myeloperoxidase homology <MPX>

Query Match 15.7%; Score 253; DB 2; Length 1535;  
Best Local Similarity 30.3%; Pred. No. 8e-11;  
Matches 80; Conservative 33; Mismatches 109; Indels 42; Gaps 13;

QY 30 SPPQILVHPDQL--FQGPGRMCRSCASGQPPPTIRWLNGQPLSMVPPDPHLLPDGT 87  
Db 367 SPPHFTQHPDQIVLHSSGHVLLDCAASGWPQDIQWFVNGRQLQSTPS-LQLQANGS 425  
QY 88 LLLLOPPARGHAGDQALSTDLGVYTCASNRRLGTAVSRGARLSVAVLRFQIOPRDMV 147  
Db 426 LILLQP-----NQLSA--GTYRCEARNSLG-SVQATARIELKELPE-ILTAPOSQT 472  
QY 148 AVVEQFTLECGPPHGPPTVSWKDGKPLALQF-----RHTVSGSLLMARAEKSD 202  
Db 473 IKGKAFVLECDAD-GNPLPTIDMQLNGVPL---PGNTPDQLENTTELVGARQSHA 528  
QY 203 XYTMCVATNSAGHRSRAARVSIQ-----PDYTEPVELLAV---RIQLENTVLLNPDP 255

Db 529 GVYRCTAHNENG-ETSVEATIKVERSQPOLAIEPSNLVAITGTIEL-----PC 578  
Qy 256 EGPKEPRAVWLXMKVSGPRLPNL 279  
Db 579 QADQPEDGLQISWRHGRLLDPNV 602

RESULT 8  
S26180  
neurofascin - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S26180  
R:Volkmmer, H.; Haesel, B.; Wolff, J.M.; Frank, R.; Rathjen, F.G.  
J. Cell Biol. 118, 149-161, 1992  
A:Title: Structure of the axonal surface recognition molecule neurofascin and its relationship to the cell adhesion molecule L1; fibronectin type III repeat homology; F;275-336/Domain: immunoglobulin homology <IMW>  
A:Reference number: S26180; MUID:92317154; PMID:1377696  
A:Accession: S26180  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1272 <VOL>  
A:Cross-references: EMBL:X65224; NID:G63659; PIDN:CAA46330.1; PID:G63660  
C:Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; F;275-336/Domain: immunoglobulin homology <IMW>

Query Match 15.6%; Score 251; DB 2; Length 1272;  
Best Local Similarity 34.5%; Pred. No. 9.1e-11;  
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 32 PQILVHPQDQLFQSPG-PARMSCRASGQPPPTIRWLNGQLPSMVPPDPHLLPDGTILL 90  
Db 355 PYWLDEPQN-LILAPGEDGLVCRANGNPKESIQWLNGEPIEGSPNPSPREVAGDTIVF 413  
Qy 91 LOPPARGHANHGQALSTDLGYVTCASNRLGTAVSRGARLSVAVLRDEFQIQPR 144  
Db 414 -----RDTQIGSS--AVYQCWASNEHGYLL-----ANAFVSVL-----DVPPRILAPRN 455  
Qy 145 DMVAVVGQFT-LEGPPWGHPEPTVSWKDGKPLALQPGHRTV-SGSLMARAEKSD 202  
Db 456 QLKVQVNRDLDC-PFGSGPIPLRFRKNGQGNLGGNYKAHENGSLMSMARKEDQ 514  
Qy 203 XYTMCVATNSAGHRESRAARVS10EP 228  
Db 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

RESULT 9  
151669  
tumor suppressor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: 151669  
R:Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, E.R.  
Dev. Biol. 166, 654-665, 1994  
A:Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the developing frog  
A:Reference number: 151669; MUID:95113183; PMID:7813784  
A:Accession: 151669  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1427 <PTE>  
A:Cross-references: EMBL:U10986; NID:G606873; PIDN:AAA70168.1; PID:G606874  
C:Genetics: XDCa  
A:Gene: XDCa

Query Match 15.2%; Score 245; DB 2; Length 1427;  
Best Local Similarity 31.0%; Pred. No. 2.9e-10;  
Matches 75; Conservative 32; Mismatches 99; Indels 36; Gaps 10;

Qy 49 ARMSCRASGQPPPTIRWLNGQLPSMVPPDPHLL-LPDGTILLLOPPARGHAHNGQALST 107  
Db 157 ALLRCETITGEMPTISWQNEEDLKVTPTGDPRLVLPSGTLOI-----SRLQTADG----- 207  
Qy 108 DLGVVTCASNRLGTAVSRGARLSVAVLRD-----FQIQPRDMVAVVGEQFTLECGP 160

Db 208 --GVYRCLAKNPGSARVGNEL--RILSSGLHRQVFLQPSNVVAIEQDQDAVLECAV 263  
Qy 161 PWGHPPTVSWKDGKPLALQPGHRTVSGS-ILMARAEKSDXYTMCVATNSAGHRESR 219  
Db 264 S-GYPTPTIWMQGDPEVPIRTKYSVLGGSNLLISNVTDDAGAYTCVATYKNTSFS 322  
Qy 220 AARVSIQEPDYTEPEVELLA---VRIQLENVTLLNPDPAEGPKPRPAVWLXMKVSGPRL 276  
Db 323 ADLTVMVPPQFLNHPANLYAESMDIEFE-----CAVSGKPSPTV--KWTQNGEVI 372  
Qy 277 PN 278  
Db 373 PS 374

RESULT 10  
TDHULK  
leukocyte antigen-related protein precursor - human  
N:Alternate names: leukocyte common antigen homolog  
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999  
C:Accession: S03841; JLO051  
R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.  
J. Exp. Med. 168, 1523-1530, 1988  
A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to protein-tyrosine-phosphatase; fibronectin type III repeat homology; F;116-1897/Domain: signal sequence #status predicted <SIG>  
A:Reference number: JLO051; MUID:89035978; PMID:2972792  
A:Accession: S03841  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1897 <STR>  
A:Cross-references: EMBL:Y00815; NID:G34266; PIDN:CAA68754.1; PID:G34267  
C:Genetics: LAR  
A:Gene: GDB:PTPRF; LAR  
A:Cross-references: GDB:120138; OMIM:179590  
A:Map position: 1p34-1p34  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; F;116-1897/Domain: signal sequence #status predicted <SIG>  
F;116-1897/Domain: signal sequence #status predicted <SIG>  
F;17-1250/Domain: extracellular #status predicted <EXT>  
F;37-99/Domain: immunoglobulin homology <IMW1>  
F;119-199/Domain: immunoglobulin homology <IMW2>  
F;236-290/Domain: immunoglobulin homology <IMW3>  
F;308-390/Domain: fibronectin type III repeat homology <FN3A>  
F;403-489/Domain: fibronectin type III repeat homology <FN3B>  
F;501-583/Domain: fibronectin type III repeat homology <FN3C>  
F;596-685/Domain: fibronectin type III repeat homology <FN3D>  
F;698-798/Domain: fibronectin type III repeat homology <FN3E>  
F;810-893/Domain: fibronectin type III repeat homology <FN3F>  
F;905-989/Domain: fibronectin type III repeat homology <FN3G>  
F;1001-1078/Domain: fibronectin type III repeat homology <FN3H>  
F;1251-1274/Domain: transmembrane #status predicted <TM>  
F;1275-1897/Domain: intracellular #status predicted <INT>  
F;1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F;1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F;1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;44-97, 146-197, 243-288/Disulfide bonds: #status predicted  
F;107, 240, 285, 711, 956/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;1538/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1544/Binding site: substrate phosphate (Arg) #status predicted  
F;1829/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 15.2%; Score 244.5; DB 1; Length 1897;  
Best Local Similarity 31.3%; Pred. No. 4.3e-10;  
Matches 73; Conservative 41; Mismatches 80; Indels 39; Gaps 10;

Qy 15 LPLLLLLIMGMAQ-----DSPQILVHPQDQLFQSPGPARMSCRASGQPPPTIRWLNGQ 70  
Db 2 VPLVPLVLMGLVAGAHGDSKPVFKVPEDQTLGSGVASFVCQATGEPKPRITWMKKGK 61

[illegible]

RESULT 13  
S50893  
Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000  
C;Accession: S50893; S40281  
R;Wagner, J.; Boerboom, D.; Tremblay, M.L.  
Eur. J. Biochem. 226, 773-782, 1994  
A;Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type  
A;Reference number: S50893; MUID:95112841; PMID:7529177  
A;Accession: S50893  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1907 <WAG>  
A;Cross-references: EMBL:X82288; NID:9587483; PIDN:CAAS7732.1; PID:9587484  
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
submitted to the EMBL Data Library, June 1993  
A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
A;Reference number: S40280  
A;Accession: S40281  
A;Molecule type: mRNA  
A;Residues: 1441-1501, E', 1503-1546 <HEN>  
A;Cross-references: EMBL:Z23050; NID:9438137; PIDN:CAA90585.1; PID:9438138  
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
ogy  
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F;145-209/Domain: immunoglobulin homology <IMM1>  
F;246-300/Domain: immunoglobulin homology <IMM2>  
F;413-506/Domain: fibronectin type III repeat homology <3FR>  
F;1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F;1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F;1664-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F;1548/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1554/Binding site: substrate phosphate (Arg) #status predicted  
F;1839/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;1845/Binding site: substrate phosphate (Arg) #status predicted

Query Match 14.8%; Score 237.5; DB 2; Length 1907;  
Best Local Similarity 30.9%; Pred. No. 1.4e-09;  
Matches 72; Conservative 40; Mismatches 82; Indels 39; Gaps 11;

Qy 13 GSPLELLLLMGMAQSPPOILVHPDQQLFQPGPARMSCRASGQPPPTIRW-----LL 67  
Db 14 -GPVGLFVLLARGCLAEPPFIREPRDQIGVSGVASFVQATGDKPRVYWNKKGKV 73

Qy 68 NQPLSVPPDPHLLPDGTLILLQPPARGHNDGQALST--DLGVYTCESNRLGTAVS 125  
Db 74 NSQRFETIDFE---SSGAVLRQP-----LRTPRDENVYECVAQNSVG-EIT 117

Qy 126 RGARLSVAVLRDEFQIOPRDVAVVVGQF-----TLFCGPPWGHPEPTVSMWKDGK 176  
Db 118 IHAKLT--VLRED-QLPPGFNIDMPQPKVETRTATMLCAAS-GNPDPEITWFKDEL 173

Qy 177 PL--ALQGR--HTVSGGSLMARAEKSDXYTMCVATNSAGHRSRAARVSIQ 226  
Db 174 PVDPSASNGRIKQLRSALQIESSEETDQKYECVATNSAGVRYSSPANLYVR 226

RESULT 14  
A34695  
axonal glycoprotein TAG-1 precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-Jun-1990 #sequence\_revision 29-Jun-1990 #text\_change 21-Jan-2000  
C;Accession: A34695  
R;Furley, A.J.; Morton, S.B.; Manalo, D.; Karagozeos, D.; Dodd, J.; Jessell, T.M.  
Cell 61, 157-170, 1990  
A;Title: The axonal glycoprotein TAG-1 is an immunoglobulin superfamily member with neur  
A;Reference number: A34695; MUID:90199890; PMID:2317872  
A;Accession: A34695  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1040 <FUR>

A;Cross-references: GB:M31725; NID:9207148; PIDN:AAA42201.1; PID:9207149  
C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology  
C;Keywords: glycoprotein  
F;343-399/Domain: immunoglobulin homology <IMM>

Query Match 14.7%; Score 236.5; DB 2; Length 1040;  
Best Local Similarity 28.2%; Pred. No. 8.7e-10;  
Matches 84; Conservative 43; Mismatches 100; Indels 71; Gaps 15;

Qy 18 LLLLLIMG-----GWAQDSP-----PQILVHPDQQLFQPGPARMSCRASG 57  
Db 11 LLLLVLATVALVSSPGWSPFAQGPATFGPIFEQPIGLLPFEE---SAEDQVTLACARA 67

Qy 58 QPPTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHNDGQALSTDLGVYTCES 117  
Db 68 SPATYRWKNGTDMLEFGSRHQLM-GGNLVIMSP-----TKTODAGVYQCLAS 116

Qy 118 NRLGTAVSRGARLSVAVLRDEFQIOPRDVAVV-VGEQFTLECGPPWGHPEPTVSMWKDGK 176  
Db 117 NPVGTVVSKAVLRFGFLQF-FSKEERDPVKTHEGVMGLPCNPPPAHYPGLSYRWLLNEF 175

Qy 177 PLAL-QGRHTVS--CGSLLMARAEKSDXYTMCVATNSAGHRE-----SRAARVSI- 225  
Db 176 PNFTPTDGRHFVSQTTGNLYIARTNASDLGNYSCLATS---HMDFTSKVSFSPAQLNLA 232

Qy 226 -QSPQDYT-----EPVELLAVRIQLENVTLNPDPAEGPKPRPAVWLXN-KVSG 272  
Db 233 AEDPRLFAPSIKARFPETVALVQQVTLFCFAGFNPVR-----IKRWKVDG 280

RESULT 15  
A49356  
transient axonal glycoprotein TAG-1 precursor - human  
N;Alternate names: axonin-1  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 23-Mar-1995 #text\_change 24-Sep-1999  
C;Accession: S35508; S28830; A49356  
R;Hasler, T.  
submitted to the EMBL Data Library, September 1992  
A;Reference number: S35508  
A;Accession: S35508  
A;Molecule type: mRNA  
A;Residues: 1-1040 <HAS>  
A;Cross-references: EMBL:X68274; NID:936674; PIDN:CAA48335.1; PID:936675  
R;Hasler, T.H.; Rader, C.; Stoekli, E.T.; Zuellig, R.A.; Sonderegger, P.  
Eur. J. Biochem. 211, 329-339, 1993  
A;Title: cDNA cloning, structural features, and eucaryotic expression of human TAG-1/axo  
A;Reference number: S28830; MUID:93145965; PMID:8425542  
A;Accession: S28830  
A;Molecule type: mRNA  
A;Residues: 1-296, 'T', 298-1040 <HA2>  
A;Cross-references: EMBL:X68274  
R;Tsotra, P.C.; Karagozeos, D.; Theodorakis, K.; Michaelidis, T.M.; Modi, W.S.; Furley,  
Genomics 18, 562-567, 1993  
A;Title: Isolation of the cDNA and chromosomal localization of the gene (TAG1) encoding  
A;Reference number: A49356; MUID:94140354; PMID:8307567  
A;Accession: A49356  
A;Molecule type: mRNA  
A;Residues: 1-1001, 'G', 1003-1040 <TSI>  
A;Cross-references: GB:X67734  
C;Genetics:  
A;Gene: GDB:TAX1  
A;Cross-references: GDB:138782  
A;Map position: 1q32-1q32  
C;Superfamily: contactin; glycoprotein  
C;Keywords: cell adhesion; signal sequence #status predicted <SIG>  
F;1-28/Domain: axonal glycoprotein TAG-1 #status predicted <MAT>  
F;29-1040/Product: axonal glycoprotein homology <IMM1>  
F;254-308/Domain: immunoglobulin homology <IMM2>  
F;341-397/Domain: immunoglobulin homology <IMM2>  
F;76,196,204,461,477,498,525,775,830,904,918,940/Binding site: carbohydrate (Asn) (coval  
Query Match 14.4%; Score 232; DB 2; Length 1040;

Best Local Similarity 28.7%; Pred. No. 1.9e-09;  
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;

QY	3	SGGDSLLGGRGSLPLLLLLIMGMAODSPQILVHPDQLFQPGPARMSCRASGQPPPT	62
Db	23	SAWSSALGSQTT-----FGPVFEDQLSLVL-FFESTEE---QVLLACRARASPPAT	70
QY	63	IRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTCESNRLGT	122
Db	71	YRWKMGTEMKLEPGSRHQLV-GGNLVINP-----TKAQDAGVYQCLASNPVGT	119
QY	123	AVSRGRLSVAVLREDFQIQPRDMV-AVVGEOFTLECGPPWGHPEPTVSWWKGKPLAL-	180
Db	120	VVSREAILRFGFLQE-FSKEERDPVKAHEGWVMLFCNPPAHYPGLSYRWLLNEFPNFIP	178
QY	181	QPCRHTVS--GGSLLMARAEKSDEXTYMCVATNSAGHRE-----SRAARVSIQ-----	226
Db	179	TGRHFVSQTTGNLYTARTNASDLGNYSCLATS---HMDFTSKSVFSKFAQLNLAAEDTR	235
QY	227	-----EPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVMLXW-KVSG	272
Db	236	LFAPSIKARPPAETVALVGOQVLECFAGFNPVPR-----IKWRKVDG	278

Search completed: January 30, 2004, 15:57:08  
Job time : 14.6529 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:45:39 ; Search time 10.4663 Seconds  
(without alignments)  
1361.423 Million cell updates/sec

Title: US-10-047-021-86

Perfect score: 1608

Sequence: 1 MGSGGDSILGGRGSLPLLL.....SGPRLPREAREILRGQRNTG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.5	15.2	1897	1 PTFP_HUMAN	P10586 homo sapien
2	236.5	14.7	1040	1 AXOI_RAT	P22063 rattus norv
3	232	14.4	1040	1 AXOI_HUMAN	Q02246 homo sapien
4	231.5	14.4	3707	1 PGBM_MOUSE	Q05793 mus musculu
5	230	14.3	1912	1 PTFP_HUMAN	P23468 homo sapien
6	223	13.9	1493	1 NEOI_HUMAN	P97798 mus musculu
7	222	13.8	2029	1 LAR_DROME	P16621 drosophila
8	221.5	13.8	1377	1 NEOI_RAT	P97603 rattus norv
9	217.5	13.5	1070	1 PTK7_HUMAN	Q13308 homo sapien
10	217.5	13.5	1461	1 NEOI_HUMAN	Q92859 homo sapien
11	215.5	13.4	1443	1 NEOI_CHICK	Q90610 gallus gall
12	214	13.3	1036	1 AXOI_CHICK	P28685 gallus gall
13	209	13.0	1447	1 DCC_MOUSE	P70211 mus musculu
14	207.5	12.9	1302	1 NRG_DROME	P20241 drosophila
15	206	12.8	1447	1 DCC_HUMAN	P43146 homo sapien
16	206	12.8	4391	1 PGBM_HUMAN	P98160 homo sapien
17	202	12.6	837	1 NCW2_MOUSE	O35136 mus musculu
18	196.5	12.2	1914	1 KMLS_HUMAN	Q13746 homo sapien
19	195.5	12.2	1091	1 NCAL_CHICK	P13590 gallus gall
20	195.5	12.2	6632	1 UN89_CAEEL	O01761 caenorhabdi
21	194.5	12.1	1284	1 NRCA_CHICK	P30331 gallus gall
22	193	12.0	837	1 NCW2_HUMAN	O15394 homo sapien
23	193	12.0	1266	1 NCAL_CHICK	Q03696 gallus gall
24	191	11.9	1260	1 CAML_MOUSE	P11627 mus musculu
25	188.5	11.7	2200	1 LAR_CAEEL	Q98m8 caenorhabdi
26	186	11.6	416	1 RAGE_BOVIN	Q28173 bos taurus
27	186	11.6	1257	1 CAML_HUMAN	P32004 homo sapien
28	185	11.5	725	1 NCW2_MOUSE	P13594 mus musculu
29	185	11.5	1115	1 NCAL_MOUSE	P13595 mus musculu
30	184.5	11.5	333	1 AMAL_DROME	P15364 drosophila
31	184	11.4	1051	1 PTK7_CHICK	Q91048 gallus gall
32	184	11.4	3375	1 UN52_CAEEL	Q05661 caenorhabdi
33	183.5	11.4	1010	1 CONT_CHICK	P14781 gallus gall

34	183	11.4	858	1 NCAL_RAT	P13596 rattus norv
35	182	11.3	1259	1 CAML_RAT	Q05695 rattus norv
36	179	11.1	2012	1 DSCA_HUMAN	O60469 homo sapien
37	176	10.9	853	1 NCAL_BOVIN	P31836 bos taurus
38	174.5	10.9	873	1 FAS2_DROME	P34082 drosophila
39	173.5	10.8	761	1 NCW2_HUMAN	P13592 homo sapien
40	173.5	10.8	848	1 NCAL_HUMAN	P13591 homo sapien
41	172	10.7	404	1 RAGE_HUMAN	Q15109 homo sapien
42	170.5	10.6	1018	1 CONT_HUMAN	Q12860 homo sapien
43	168	10.4	1021	1 CONT_RAT	Q63198 rattus norv
44	167.5	10.4	912	1 ICAS_RABIT	Q28730 oryctolagus
45	165.5	10.3	1020	1 CONT_MOUSE	P12960 mus musculu

#### ALIGNMENTS

##### RESULT 1

PTFP\_HUMAN  
ID PTFP\_HUMAN STANDARD; PRT; 1897 AA.  
AC P10586;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).  
GN PTFP OR LAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Tonsil;  
RX MEDLINE=89035978; PubMed=2972792;  
RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;  
RT "A new member of the immunoglobulin superfamily that has a  
cytoplasmic region homologous to the leukocyte common antigen.";  
RL J. Exp. Med. 168:1523-1530(1988).  
RN [2]  
RP MUTAGENESIS.  
RX MEDLINE=90046860; PubMed=2554325;  
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
RT "A family of receptor-linked protein tyrosine phosphatases in humans  
and Drosophila.";  
RN [3]  
RP proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
RN [3]  
RP MUTAGENESIS.  
RX MEDLINE=90316093; PubMed=1695146;  
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;  
RT "Distinct functional roles of the two intracellular phosphatase like  
domains of the receptor-linked protein tyrosine phosphatases LCA and  
LAR.";  
RL EMBO J. 9:2399-2407(1990).  
CC -!- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.  
IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY  
(PTPASE).  
CC -!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE  
THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE  
FIRST ONE.  
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
tyrosine + phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 8 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.  
-----  
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or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).

```
CC EMBL; Y00815; CAA68754.1; -.
DR PIR; S03841; TDHULK.
DR PDB; 1LAR; 25-APR-00.
DR Genew; HGNC:9670; PTPRF.
DR MIM; 179590; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. .; TAS.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 7.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00700; PTPPHPTASE.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00835; IG-LIKE; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 1897
FT DOMAIN 17 1250
FT TRANSMEM 1251 1274
FT DOMAIN 1275 1897
FT DOMAIN 123 113
FT DOMAIN 125 214
FT DOMAIN 222 304
FT DOMAIN 1360 1606
FT DOMAIN 1649 1897
FT ACT SITE 1538 1538
FT ACT SITE 1829 1829
FT CARBOHYD 107 107
FT CARBOHYD 240 240
FT CARBOHYD 285 285
FT CARBOHYD 711 711
FT CARBOHYD 956 956
FT MUTAGEN 1538 1538
FT SEQUENCE 1897 AA; 211844 MW; 439850F1D5C031FF CRC64;

Query Match 15.2%; Score 244.5; DB 1; Length 1897;
Best Local Similarity 31.3%; Pred. No. 1e-10;
Matches 73; Conservative 41; Mismatches 80; Indels 39; Gaps 10;

Qy 15 LPLLILLMGWAQ----DSPQLVHPQDQLFOGPGPARMSCRASGPPPTIIRLLNGQ 70
Db 2 VLPVFLVNLGLVAGAGHGSFVKIKVPEDQTLGSGVASFVCQATGPKPRITIMKKKG 61
Qy 71 PLS-----MVPDPDHLHLDGTLTLLQPPARGHAGDQALSTDLGVYTCEASNRIGTAVS 125
Db 62 KVSSQRFVEIFDD-----GAGSVLRIQP-----LRVQDEAIVECTATNSLG-EIN 107
Qy 126 RGARLSAVLREDFOIQPRDMVAVVGEQF-----TLGCGPWHGHPETVSNWKDGK 176
Db 108 TSAKLSVL---EEQLPFGFSDMGPPQPKVKVKARTATMLCA-AGGNPDPEISWFKDFL 163
Qy 177 PL--ALQGR-HTVSGGSLMARAEKSDXTVMCVATNSAGHRSRAARVSIQ 226
Db 164 PVDPATSNRIKQLRSGALQIESSESDQGYKECVATNSAGTRYSAFANLYVR 216

RESULT 2
```

```
AXO1 RAT
ID AXO1 RAT STANDARD; PRT; 1040 AA.
AC P22063;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Contactin 2 precursor (Axonin-1) (Axonal glycoprotein TAG-1)
DE (Transient axonal glycoprotein 1) (TAX-1).
GN CNTN2 OR TAXI
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-41.
RC TISSUE=spinal cord;
RX MEDLINE=9019890; PubMed=2317872;
RA Furlley A.J., Morton S.B., Manalo D., Karagozeos D., Dodd J.,
RA Jessell T.M.;
RT "The axonal glycoprotein TAG-1 is an immunoglobulin superfamily
member with neurite outgrowth-promoting activity.";
RL Cell 61:157-170(1990).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE INITIAL GROWTH AND GUIDANCE OF
AXONS. MAY BE INVOLVED IN CELL ADHESION.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A
GPI-ANCHOR AND IS ALSO RELEASED FROM NEURONS.
CC -1- TISSUE SPECIFICITY: IN NEURAL TISSUES IN EMBRYOS, AND IN ADULT
BRAIN, SPINAL CORD AND CEREBELLUM.
CC -1- DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED ON A SUBSET OF AXONS
IN THE DEVELOPING RAT NERVOUS SYSTEM.
CC -1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains..
CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
CC
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CC
CC EMBL; M31725; AAA42201.1; -.
DR PIR; A34695; A34695.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; ig; 6.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00835; IG-LIKE; 6.
KW Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;
KW Cell adhesion; Repeat;
FT SIGNAL 1 30
FT CHAIN 31 1015
FT PROPEP 1016 1040
FT DOMAIN 39 130
FT DOMAIN 135 224
FT DOMAIN 241 324
FT DOMAIN 329 413
FT DOMAIN 419 506
FT DOMAIN 511 605
FT DOMAIN 608 614
FT DOMAIN 613 708
FT DOMAIN 716 811
FT DOMAIN 818 910
FT DOMAIN 911 1005
FT SITE 796 798
FT CARBOHYD 78 78
FT CARBOHYD 200 200
FT
```



Query Match 14.4%; Score 232; DB 1; Length 1040;  
Best Local Similarity 28.7%; Pred. No. 4.6e-10;  
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;

```
QY 3 SGGSLGGRGSLPLLLILLMGMAQSPPOILVHPDQLFQGGPARMSCRAGSQPPPT 62
DB 23 SAMSALGSQTT-----FGPVFEOPLSVL-FPESTEE---QVLLACRASPAT 70
QY 63 IRWLLNGOPLSMVPPDPHLLPDGTLTLLLOPPARGHAHDGQALSTDLGVYTCEASNLGT 122
DB 71 YRWKXNGTEMKLEPGSRHQLV-GGNLVIMNP-----TKAQDAGVYQCLASNPVGT 119
QY 123 AVSFCARLSVAVLREDFQIQPRDMV-AVVGQFTLECGPPGHPEPTVSMWCKGLAL- 180
DB 120 VVSREAILRFLGLOE-FSKEREDPKAHEGVGWLPCNPPAHYFGLSTYRWLLNEFPNIP 178
QY 181 QPGRHTVS--GGSLIMARAESDXTYMCVATNSAGHRE-----SRAARVSIQ----- 226
DB 179 TDGRHFVSQTTGNLYARTNASDLGNYSCLATS-----HMDFTKSVFSKFAQLNLAEDTR 235
QY 227 -----EPQDYTEPVELLAVRIQIENVTLNPDPAEGPKPRPAVLWX-KVSG 272
DB 236 LFAPSIKARPAETAYLVGQQVTLCEFAFGNFPVR-----IKWRKVDG 278
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## RESULT 4

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PFGBM MOUSE STANDARD; PRT; 3707 AA.
ID PQ5793;
AC Q05793;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=92078153; PubMed=1744087;
RA Noonan D.M., Fullie A., Valente P., Cai S., Horigan E., Sasaki M.,
RA Yamada Y., Hassell J.R.;
RT "The complete sequence of perlecan, a basement membrane heparan
RT sulfate proteoglycan, reveals extensive similarity with laminin A
RT chain, low density lipoprotein-receptor, and the neural cell adhesion
RT molecule."
RL J. Biol. Chem. 266:22939-22947(1991).
RN [2]
RP SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89034110; PubMed=2972708;
RA Noonan D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M.,
RA Yamada Y., Hassell J.R.;
RT "Identification of cDNA clones encoding different domains of the
RT basement membrane heparan sulfate proteoglycan."
RL J. Biol. Chem. 263:16379-16387(1998).
CC -!- FUNCTION: This protein is an integral component of basement
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
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CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 15 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M77174; AAA39911.1; -
CC EMBL; J04054; AAA39899.1; -
CC EMBL; J04055; AAA39912.1; -
CC PIR; S18252; S18252.
CC PDB; 1GL4; 28-NOV-01.
CC MGD; MGI:96257; Hspg2.
CC GO; GO:0005604; C:basement membrane; IDA.
CC GO; GO:0008104; P:protein localization; IMP.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig C2.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR002172; LDL receptor_A.
CC InterPro; IPR000082; SEA_domain.
CC Pfam; PF00008; EGF; 4.
CC Pfam; PF00047; Ig; 15.
CC Pfam; PF00052; laminin_B; 3.
CC Pfam; PF00053; laminin_EGF; 7.
CC Pfam; PF00054; laminin_G; 3.
CC Pfam; PF00057; ldl_recept_a; 4.
CC Pfam; PF01390; SEA; 1.
CC PRINTS; PR00261; LDLRECEPTOR.
CC ProDom; PD003031; Laminin_B; 3.
CC SMART; SM00180; EGF_Lam; 7.
CC SMART; SM00408; IGG2; 14.
CC SMART; SM00281; Lamb; 3.
CC SMART; SM00282; LamG; 3.
CC SMART; SM00192; LDLa; 4.
CC SMART; SM00200; SEA; 1.
CC PROSITE; PS00022; EGF_1; 8.
CC PROSITE; PS01186; EGF_2; 5.
CC PROSITE; PS50835; IG LIKE; 15.
CC PROSITE; PS50025; LAM_G DOMAIN; 3.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
CC PROSITE; PS01209; LDLRA_1; 4.
CC PROSITE; PS50068; LDLRA_2; 4.
CC PROSITE; PS50024; SEA; 1.
CC Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
CC Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
CC Extracellular matrix; EGF-like domain; 3D-structure.
CC SIGNAL 1 21
CC CHAIN 22 3707
CC DOMAIN 80 194
CC LDL-RECEPTOR CLASS A 1.
CC LDL-RECEPTOR CLASS A 2.
CC LDL-RECEPTOR CLASS A 3.
CC LDL-RECEPTOR CLASS A 4.
CC IG-LIKE C2-TYPE 1.
CC LAMININ EGF-LIKE 1 (N-TERMINAL).
CC LAMININ DOMAIN IV 1 (DOMAIN III A).
CC LAMININ EGF-LIKE 1 (C-TERMINAL).
CC LAMININ EGF-LIKE 2.
CC LAMININ EGF-LIKE 3.
CC LAMININ EGF-LIKE 4 (INCOMPLETE).
CC SIGNAL 22 3707
CC DOMAIN 195 234
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CC LAMININ DOMAIN IV 1 (DOMAIN III A).
CC LAMININ EGF-LIKE 1 (C-TERMINAL).
CC LAMININ EGF-LIKE 2.
CC LAMININ EGF-LIKE 3.
CC LAMININ EGF-LIKE 4 (INCOMPLETE).
CC SIGNAL 22 3707
CC DOMAIN 195 234
CC LDL-RECEPTOR CLASS A 1.
CC LDL-RECEPTOR CLASS A 2.
CC LDL-RECEPTOR CLASS A 3.
CC LDL-RECEPTOR CLASS A 4.
CC IG-LIKE C2-TYPE 1.
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CC LAMININ DOMAIN IV 1 (DOMAIN III A).
CC LAMININ EGF-LIKE 1 (C-TERMINAL).
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CC LAMININ EGF-LIKE 3.
CC LAMININ EGF-LIKE 4 (INCOMPLETE).
CC SIGNAL 22 3707
CC DOMAIN 195 234
CC LDL-RECEPTOR CLASS A 1.
CC LDL-RECEPTOR CLASS A 2.
CC LDL-RECEPTOR CLASS A 3.
CC LDL-RECEPTOR CLASS A 4.
CC IG-LIKE C2-TYPE 1.
CC LAMININ EGF-L
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DOMAIN 924 933 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 934 1125 LAMININ DOMAIN IV 2 (DOMAIN III B).  
FT DOMAIN 1126 1158 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 1159 1208 LAMININ EGF-LIKE 6.  
FT DOMAIN 1209 1255 LAMININ EGF-LIKE 7.  
FT DOMAIN 1275 1324 LAMININ EGF-LIKE 8.  
FT DOMAIN 1325 1334 LAMININ EGF-LIKE 9 (N-TERMINAL).  
FT DOMAIN 1335 1529 LAMININ DOMAIN IV 3 (DOMAIN III C).  
FT DOMAIN 1530 1612 LAMININ EGF-LIKE 9 (C-TERMINAL).  
FT DOMAIN 1563 1621 LAMININ EGF-LIKE 10.  
FT DOMAIN 1613 1670 LAMININ EGF-LIKE 11.  
FT DOMAIN 1677 1771 IG-LIKE C2-TYPE 2.  
FT DOMAIN 1772 1865 IG-LIKE C2-TYPE 3.  
FT DOMAIN 1866 1954 IG-LIKE C2-TYPE 4.  
FT DOMAIN 1955 2049 IG-LIKE C2-TYPE 5.  
FT DOMAIN 2050 2148 IG-LIKE C2-TYPE 6.  
FT DOMAIN 2149 2244 IG-LIKE C2-TYPE 7.  
FT DOMAIN 2245 2343 IG-LIKE C2-TYPE 8.  
FT DOMAIN 2344 2436 IG-LIKE C2-TYPE 9.  
FT DOMAIN 2437 2532 IG-LIKE C2-TYPE 10.  
FT DOMAIN 2533 2619 IG-LIKE C2-TYPE 11.  
FT DOMAIN 2620 2720 IG-LIKE C2-TYPE 12.  
FT DOMAIN 2721 2809 IG-LIKE C2-TYPE 13.  
FT DOMAIN 2810 2895 IG-LIKE C2-TYPE 14.  
FT DOMAIN 2896 2980 IG-LIKE C2-TYPE 15.  
FT DOMAIN 2981 3162 LAMININ G-LIKE 1.  
FT DOMAIN 3163 3241 EGF-LIKE.  
FT DOMAIN 3242 3425 LAMININ G-LIKE 2.  
FT DOMAIN 3426 3705 LAMININ G-LIKE 3.  
FT DOMAIN 3706 3795 HEPARAN SULFATE (POTENTIAL).  
FT SITE 65 67 HEPARAN SULFATE (POTENTIAL).  
FT SITE 71 73 HEPARAN SULFATE (POTENTIAL).  
FT SITE 76 78 MEDIATES MOTOR NEURON ATTACHMENT  
FT SITE 3615 (POTENTIAL).  
FT DISULFID 199 212 BY SIMILARITY.  
FT DISULFID 206 225 BY SIMILARITY.  
FT DISULFID 219 234 BY SIMILARITY.  
FT DISULFID 285 297 BY SIMILARITY.  
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FT DISULFID 388 403 BY SIMILARITY.  
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FT DISULFID 764 773 BY SIMILARITY.  
FT DISULFID 766 780 BY SIMILARITY.  
FT DISULFID 783 792 BY SIMILARITY.  
FT DISULFID 795 811 BY SIMILARITY.  
FT DISULFID 814 829 BY SIMILARITY.  
FT DISULFID 816 839 BY SIMILARITY.  
FT DISULFID 842 851 BY SIMILARITY.  
FT DISULFID 854 869 BY SIMILARITY.  
FT DISULFID 1159 1168 BY SIMILARITY.  
FT DISULFID 1161 1175 BY SIMILARITY.  
FT DISULFID 1178 1187 BY SIMILARITY.  
FT DISULFID 1190 1206 BY SIMILARITY.  
FT DISULFID 1209 1224 BY SIMILARITY.  
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FT DISULFID 1237 1246 BY SIMILARITY.  
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FT DISULFID 1275 1287 BY SIMILARITY.  
FT DISULFID 1277 1293 BY SIMILARITY.  
FT DISULFID 1299 1304 BY SIMILARITY.  
FT DISULFID 1307 1322 BY SIMILARITY.  
FT DISULFID 1322 1352 BY SIMILARITY.  
FT DISULFID 1563 1572 BY SIMILARITY.  
FT DISULFID 1565 1579 BY SIMILARITY.  
FT DISULFID 1582 1591 BY SIMILARITY.  
FT DISULFID 1594 1610 BY SIMILARITY.  
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FT DISULFID 1615 1638 BY SIMILARITY.

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FT DISULFID 1792 1819 BY SIMILARITY.  
FT DISULFID 1886 1932 BY SIMILARITY.  
FT DISULFID 2021 2021 BY SIMILARITY.  
FT DISULFID 2073 2118 BY SIMILARITY.  
FT DISULFID 2170 2215 BY SIMILARITY.  
FT DISULFID 2268 2313 BY SIMILARITY.  
FT DISULFID 2365 2413 BY SIMILARITY.  
Query Match 14.4%; Score 231.5; DB 1; Length 3707;  
Best Local Similarity 27.7%; Pred. No. 2e-09;  
Matches 76; Conservative 37; Mismatches 88; Indels 73; Gaps 14;  
QY 25 GMAOD-----SPPQILVHPDQDLFOGPGPARM-----SCRASGQPPPTIRWLLNGOP 71  
DB 2420 GMAQSVNLSVHGPGPTVSVP-----EGPVHVVKMKDITLBCISSGEPSPRTRLGIP 2474  
QY 72 LSMVP-----PDPHLLPDGTLTLLLPARGHAGDQALSTDLGVYTCASNRLGTA--- 123  
DB 2475 VKLEPRMFGMLNSHML---KIASVKP-----SDAGTYVCQAQNALGTAQKQ 2518  
QY 124 ----VSRCARLSVAVLREDFOIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLA 179  
DB 2519 VELIVDTG---TVAPGTQVQVESELTLEAGTATLHCSAT-GNPPPTIHWKSLRAPL- 2573  
QY 180 LQGRHTVSGSLLMARAESDXTYMCVATNSAGHRESRAARVSIQSPQDVT----- 232  
DB 2574 --PWHRIEGTLVPRVAQDQSGQYICNATNSAGHTEATTV-LHVESPPYATIPIEHTS 2630  
QY 233 -EPVELLAVRIQLENNVTLLNPDPAEGPKPRPAVW 265  
DB 2631 AQPGLN----VOLQCL-----AHGTPPLTYQW 2653  
RESULT 5  
PTPD HUMAN STANDARD; PRT; 1912 AA.  
AC P23458;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Protein-tyrosine phosphatase delta precursor (BC 3.1.3.48) (R-PTP-delta)  
GN PTPRD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.  
RX MEDLINE=95204468; PubMed=7896816;  
RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;  
RT "Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta. Evidence for tissue-specific expression of alternative human transmembrane protein-tyrosine phosphatase delta isoforms";  
RT J. Biol. Chem. 270:6722-6728(1995).  
RN [2]  
RP SEQUENCE OF 390-1912 FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=91006018; PubMed=2170109;  
RA Krueger N.X., Streuli M., Saito H.;  
RT "Structural diversity and evolution of human receptor-like protein tyrosine phosphatases";  
RL EMBO J. 9:3241-3252(1990).  
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS;  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist;  
CC Name=1;





FT	VARSPUBLIC	863	878	/FTid=VSP_002594. Missing (in isoform 3).
FT	VARSPUBLIC	1086	1096	/FTid=VSP_002595. Missing (in isoform 4).
FT	VARSPUBLIC	1279	1331	/FTid=VSP_002596. Missing (in isoform 5).
FT	VARSPUBLIC	1493	AA;	/FTid=VSP_002597.
FT	SEQUENCE	163159	MW;	441D8519D5E17C0E CRC64;
Query Match		13.9%;	Score 223;	DB 1; Length 1493;
Best Local Similarity		29.6%;	Pred. No. 3.3e-09;	
Matches		74;	Conservative 32;	Mismatches 104; Indels 40; Gaps 18;
QY	15	LPLLLL---	IMGMAQDSPQ-----	ILVHPQDQLFQGGPARMSCRAS 56
DB	29	LPLLLLLGPASGAATK	SGPRSQSGASVRTPTFPFV	LPVDPVTLVSRGSSVILNCsAY 88
QY	57	GQPPPTIRLLNGQPL	SMVPPDPHLLPDGTL	LLQLPPARGHAHQALSTDLGVTCEA 116
DB	89	SESPNIEWKKDGTFL	NLESDRRQLLPGLSP	ISINVHSHKN-----KPDGFGVQCVa 142
QY	117	S-NRLGTAVSRGARLS	VAVLREDFQIQPRDM	VAVGEQFTLEGPPWGHPE-----PTV 169
DB	143	TVDNLTGTVSR	TAKLTVAGLPR-FTSQ	PESSVYVGNsAILNC-----EVNADLVPFV 194
QY	170	SNWKGKQPLALQGR	HTVGGSLLMARAKSD	EXTYMCVATNAGHRESRAARVSI-QEP 228
DB	195	RWEQNRQPLLLDR	IVKLPSPGTLVIGNA	TGEGDGLYRCIVESGGPKFSEABLKVQLQDP 254
QY	229	QDYTEPVELL 238		
DB	255	EEIVDLVFLM 264		
RESULT 7				
LAR_DROME				
ID	LAR_DROME	STANDARD;	PRT;	2029 AA.
AC	P16621;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Protein-tyrosine phosphatase Lar precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase) (DLAR).			
GN	DLAR.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxId=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90046860; PubMed=2554325;			
RA	Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;			
RT	"A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila."			
RL	and Drosophila."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Canton-S;			
RX	MEDLINE=96178473; PubMed=8598047;			
RA	Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,			
RA	Saito H.;			
RT	"The transmembrane tyrosine phosphatase DLAR controls motor axon guidance in Drosophila."			
RL	Cell 84:611-622(1996).			
CC	-1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.			
CC	IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.			
CC	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.			





	Query Match	13.5%; Score 217.5; DB 1;	Length 1070;
	Best Local Similarity	29.2%; Pred.No. 5.9e-09;	
	Matches	63; Conservative 35; Mismatches 93; Indels 25; Gaps 7;	
QY	26 MAQDSPPQLVLVHQDOLFQGPGFARMSCRASGQPPTIRWLLNGQPLSMVPDPDH----	80	
Dd	219 IADESFARVVLAQQDVVVARYEEAMTHFCQAQFPFSLQWLFEDEFTITNRSRPPHLRA	278	
QY	81 HLLPDGTLLLQPPARGHAHDGOALSTDLGVYYTCEASNLIGTVARSGARLSVAFLREDFQ	140	

DR MIM; 601907; --  
DR GO; 0005887; C: integral to plasma membrane; TAS.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR003962; FNII subd.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG C2.  
DR Pfam; PF00041; fn3; 6.  
DR Pfam; PF00047; IG; 4.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00060; FN3; 6.  
DR SMART; SM00408; IGC2; 3.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;  
KW Glycoprotein; Alternative splicing.  
FT SIGNAL 1 33  
FT CHAIN 34 1461  
FT DOMAIN 34 1105  
FT TRANSMEM 1106 1126  
FT DOMAIN 1127 1461  
FT DOMAIN 52 141  
FT DOMAIN 152 238  
FT DOMAIN 243 336  
FT DOMAIN 341 426  
FT DOMAIN 436 533  
FT DOMAIN 536 629  
FT DOMAIN 630 729  
FT DOMAIN 735 829  
FT DOMAIN 850 950  
FT DOMAIN 951 1052  
FT DOMAIN 1118 1121  
FT DISULFID 74 129  
FT DISULFID 173 221  
FT DISULFID 270 320  
FT DISULFID 362 410  
FT CARBOHYD 73 73  
FT CARBOHYD 210 210  
FT CARBOHYD 326 326  
FT CARBOHYD 470 470  
FT CARBOHYD 489 489  
FT CARBOHYD 639 639  
FT CARBOHYD 715 715  
FT CARBOHYD 909 909  
FT VARSPLIC 1248 1300  
FT CONFLICT 168 168  
FT SEQUENCE 1461 AA; 159958 MW; 7AAE897E69635A21 CRC64;  
Query Match 13.5%; Score 217.5; DB 1; Length 1461;  
Best Local Similarity 22.6%; Pred. No. 8.3e-09;  
Matches 86; Conservative 40; Mismatches 122; Indels 133; Gaps 11;  
QY 17 LLLLLL-----GMAQDPP-----QILVHPDQLFQGPGRMCRAS 56  
DB 18 LYCLLLGRAPGAAARSGAPQSGASIRFTPTFLVPEVDLTLSVRGSSVILNCAY 77  
QY 57 GPPPTIRWLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEA 116  
DB 78 SEPSKIEWKDGTTFLNLSVDRRLPDGSLFISNVHNRN-----KPDGYIQCA 131  
QY 117 S-NRLGTAVSRGALSVA-----133  
DB 132 TVESLGTIISRTAKLIVAGLPRTSQPEBSSVYAGNALLCEVNADLVFPVFWQNRQP 191  
QY 134 VLRED-----F 139  
DB 192 LLLDDRVIKPSGLMVISNATEGDGLYRCVVGSGPPKYSDEVKLVLPDPDEVISDLVF 251  
QY 140 QIQPRDMVAVCEQFTLECGPWGHEPTVSWKDGKPLALQPGHVT--SGSLLMARA 197  
DB 252 LKQPSPLRVIGQDVVLPVAVS-GLPTPTIKMKNEALDTSESRLLVLAGGSLEISDV 310  
QY 198 EKSDXTYMCVATNSAGHSRAARVSIOEPQDYTEPVELLAVRIQLENVTLNPDPAEG 257

Db 311 TEDDAGTYFCIADNGNETIEAQLTVOAQPEFLKQPTNIYA----HESMDIVFECEVTG 366  
QY 258 PKPRPAVLWKVSGPXLPLN 278  
Db 367 -KPTPTV--KVVKNGDMVIPS 384  
RESULT 11  
NEOL\_CHICK  
ID NEOL\_CHICK STANDARD; PRT; 1443 AA.  
AC Q90610;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Neogenin (Fragment)  
OS Gallus gallus (Chicken)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=white legorn; TISSUE=Embryonic brain;  
RX MEDLINE=95105243; PubMed=7806578;  
RA Vielmetter J., Roman J.M., Dreyer W.J.;  
RT "Neogenin, an avian cell surface protein expressed during terminal  
neural differentiation, is closely related to the human tumor  
suppressor molecule deleted in colorectal cancer.";  
RL J. Cell Biol. 127:2009-2020(1994).  
CC -!- FUNCTION: MAY BE INVOLVED AS A REGULATORY PROTEIN IN THE  
TRANSITION OF UNDIFFERENTIATED PROLIFERATING CELLS TO THEIR  
DIFFERENTIATED STATE. MAY ALSO FUNCTION AS A CELL ADHESION  
MOLECULE IN A BROAD SPECTRUM OF EMBRYONIC AND ADULT TISSUES.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- DEVELOPMENTAL STAGE: IN RETINA, EXPRESSED ON GANGLION CELL FIBERS  
AS SOON AS THEY BEGIN TO EXTEND THEIR AXONS.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC  
SUBFAMILY.  
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.  
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
EMBL; U07644; AAC59662.1; --  
DR PIR; I50600; I50600.  
DR HSPF; P11276; 2MFN.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR003962; FNII subd.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG C2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 6.  
DR Pfam; PF00047; IG; 4.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00060; FN3; 6.  
DR SMART; SM00408; IGC2; 2.  
DR PROSITE; PS50835; IG LIKE; 4.  
KW Cell adhesion; Repeat; Transmembrane; Immunoglobulin domain;  
KW Glycoprotein.  
FT NON TER 1 1090  
FT DOMAIN <1 1090  
FT TRANSMEM 1091 1111  
FT DOMAIN 1112 1443  
FT DOMAIN 118 113  
FT DOMAIN 118 204  
FT DOMAIN 212 302  
EXTRACELLULAR (POTENTIAL).  
POTENTIAL.  
CYTOPLASMIC (POTENTIAL).  
IG-LIKE C2-TYPE 1.  
IG-LIKE C2-TYPE 2.  
IG-LIKE C2-TYPE 3.

FT DOMAIN 307 392 IG-LIKE C2-TYPE 4.  
FT DOMAIN 422 519 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 522 615 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 616 714 FIBRONECTIN TYPE-III 3.  
FT DOMAIN 720 814 FIBRONECTIN TYPE-III 4.  
FT DOMAIN 835 935 FIBRONECTIN TYPE-III 5.  
FT DOMAIN 936 1037 FIBRONECTIN TYPE-III 6.  
FT DISULFID 40 95 BY SIMILARITY.  
FT DISULFID 139 187 BY SIMILARITY.  
FT DISULFID 236 286 BY SIMILARITY.  
FT DISULFID 328 376 BY SIMILARITY.  
FT CARBOHYD 39 39 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 475 475 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 625 625 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 700 700 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 894 894 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 1443 AA; 158050 MW; 558C6795579C0E26 CRC64;  
Query Match 13.4%; Score 215.5; DB 1; Length 1443;  
Best Local Similarity 31.4%; Pred. No. 1.2e-08;  
Matches 80; Conservative 27; Mismatches 117; Indels 31; Gaps 9;  
Qy 30 SPQQLVHPQDLFGPGPARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 89  
Db 17 TFFYFLVPMDLISVRGASVIMNCSSCYCTPKIEWKKGDTLLNLVSDRRQLLPDGSLL 76  
Qy 90 LLQPPARGHAHQALSTDLGYTTCAS-NRLGTAVSRGARSVAVLREDFQIQPRDMVA 148  
Db 77 INSVHSHN-----KDEGYQCVATVESIGSIVSRTAKLTAGLPR-FTSQPELSSV 129  
Qy 149 VVGQFTLECPGWHP-----PTVSWKDGKPLALQPGRHVTVSGSLLMARAEKSD 202  
Db 130 YKGSAILNC-----EVNVDLAPFVRWEQDQPLSDRVFKLPSGALLIGNATDTDG 182  
Qy 203 XYTMCVATNSAGHRSRAARVSIQEPQDYTPVELLAVR--IQLENTVLLN---PDPREG 257  
Db 183 GFYRCVIESGGTPKYSERAEKIL--PDPERQSLVFRQPSLSLTKVTGQNAVFPVCAGG 240  
Qy 258 PKPREAVLXWKVSG 272  
Db 241 ---PFTPVRTKNG 252

## RESULT 12

ID AXOI CHICK STANDARD; PRT; 1036 AA.  
AC P28685;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Contactin 2 precursor (Axonin-1).  
GN CNTN2.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92174998; PubMed=1311675;  
RA Zuellig R.A., Rader C., Schroeder A., Kalousek M.B.,  
RA von Bohlen Und Halbach F., Osterwalder T., Inan C., Stoeckli E.T.,  
RA Affolter H.-U., Fritz A., Hafen E., Sonderegger P.;  
RT "The axonally secreted cell adhesion molecule, axonin-1. Primary  
RT structure, immunoglobulin-like and fibronectin-type-III-like domains  
RT and glycosyl-phosphatidylinositol anchorage.";  
RL Eur. J. Biochem. 204:453-463(1992).  
CC -1- FUNCTION: AXON-ASSOCIATED CELL ADHESION MOLECULE (AXCAM) WHICH  
CC PROMOTES NEURITE OUTGROWTH BY INTERACTION WITH THE AXCAM L1 (G4)

CC CC OF NEURITIC MEMBRANE.  
CC CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE NEURONAL MEMBRANE BY A  
CC CC GPI-ANCHOR.  
CC CC -1- PTM: The N-terminus is blocked.  
CC CC -1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.  
CC CC -1- SIMILARITY: Contains 4 fibronectin type III domains.  
CC CC -----  
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC CC -----  
CC CC EMBL; X63101; CAA44815.1; -;  
CC CC PIR; S22383; S22383.  
CC CC PDB; 1CS6; 19-MAY-00.  
CC CC InterPro; IPR003961; FN III.  
CC CC InterPro; IPR007110; Ig-like.  
CC CC InterPro; IPR003598; Ig\_C2.  
CC CC InterPro; IPR003006; Ig\_MHC.  
CC CC Pfam; PF00041; fn3; 3.  
CC CC Pfam; PF00047; Ig; 6.  
CC CC SMART; SM00060; FN3; 4.  
CC CC SMART; SM00408; IgC2; 5.  
CC CC PROSITE; PS00835; IG-LIKE; 6.  
CC CC Immunoglobulin domain; Glycoprotein; Signal; GPI-anchor;  
CC CC Cell adhesion; Repeat; 3D-structure.  
CC CC SIGNAL 1 23 OR 25 (POTENTIAL).  
CC CC CHAIN 24 ? CONTACTIN 2.  
CC CC PROPEP 2 1036 REMOVED IN MATURE FORM.  
CC CC DOMAIN 32 123 IG-LIKE C2-TYPE 1.  
CC CC DOMAIN 128 223 IG-LIKE C2-TYPE 2.  
CC CC DOMAIN 234 317 IG-LIKE C2-TYPE 3.  
CC CC DOMAIN 322 406 IG-LIKE C2-TYPE 4.  
CC CC DOMAIN 412 499 IG-LIKE C2-TYPE 5.  
CC CC DOMAIN 504 598 IG-LIKE C2-TYPE 6.  
CC CC DOMAIN 599 608 HINGE (POTENTIAL).  
CC CC DOMAIN 601 607 GLY/PRO-RICH.  
CC CC DOMAIN 608 709 FIBRONECTIN TYPE-III 1.  
CC CC DOMAIN 710 811 FIBRONECTIN TYPE-III 2.  
CC CC DOMAIN 812 912 FIBRONECTIN TYPE-III 3.  
CC CC DOMAIN 913 1009 FIBRONECTIN TYPE-III 4.  
CC CC CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 472 472 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 493 493 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 520 520 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 770 770 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 900 900 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC CARBOHYD 914 914 N-LINKED (GLCNAC. .) (POTENTIAL).  
CC CC SEQUENCE 1036 AA; 113301 MW; 08B80143BE779794 CRC64;  
Query Match 13.3%; Score 214; DB 1; Length 1036;  
Best Local Similarity 28.7%; Pred. No. 1e-08;  
Matches 81; Conservative 40; Mismatches 107; Indels 54; Gaps 16;  
Qy 9 LGGRG-----SLPLLLLI-----MGNAQDPPQILVHPQDLF-QGPGPAR--MSCRAS 56  
Db 1 MGGTAARICTSLAVIICVNVCAQSGM-RSYGVPFEEQPAHTLFPESAEKVTLCRAR 59  
Qy 57 GQPPPTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQLPPARGHAHQALSTDLGYTTC 116  
Db 60 ANPPATYRWKNGTELKX-GPDSRYRLVAGDLVSNP-----VKANDAGSYQCVA 108  
Qy 117 SNRLGTAVSRGARSVAVLREDFQIQPRDMVAV---GEQFTLECGPPWHPPTVSMWK 173  
Db 109 TNARGTVVSREASLRFQFLQE-FSAERDPPVKITGEGVMFT--CSPPHPALSYRWLL 165  
Qy 174 DGKPLAL-QPGRHTVS--GGSLLMARAEKSDXTYMCVATNSAGHRE-----SRAARV 223



```
Db 166 NEFPNFIADGRFRVSTGNLYIAKTEASDLGNVSCFATS---HIDFITKSVFQSQL 222
Qy 224 SI--QEPQDTEPVE-----LLAVRIQLENTVLTNPDP 254
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 223 SLAEDARQAPSIKAPADYALTQGVTLCEAFGPNVP 264
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
DCC_MOUSE
ID DCC_MOUSE STANDARD; PRT; 1447 AA.
AC P70211;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor suppressor protein DCC precursor.
GN DCC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=96112625; PubMed=8570174;
RA Cooper H.M., Ames P., Britto J., Gad J., Wilks A.F.;
RT "Cloning of the mouse homologue of the deleted in colorectal cancer
RT gene (mDCC) and its expression in the developing mouse embryo.";
RL Oncogene 11:2243-2254(1995).
RN [2]
RP REVISIONS.
RC STRAIN=BALB/c; TISSUE=Brain;
RA Cooper H.M.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P70211-1; Sequences=VSP 002501;
CC Note-Isoform B is produced by alternative initiation at Met-85
CC of isoform A;
CC Name=C;
CC IsoId=P70211-2; Sequences=VSP 002501;
CC Event-Alternative initiation;
CC Comment=2 isoforms, A (shown here) and B, are produced by
CC alternative initiation at Met-1 and Met-85;
CC -!- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE
CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN
CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.
CC -!- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS
CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION
CC AND REMAIN AT THIS LEVEL IN THE ADULT.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. DCC
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.
CC
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CC use by non-profit institutions as long as its content is in no way
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DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00047; Ig; 4.
DR PRINTS; PR00014; ENTYPBIII.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00408; IGE2; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
KW Glycoprotein; Immunoglobulin domain; Transmembrane; Signal;
KW Repeat; Anti-oncogene; Alternative initiation; Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 1447
FT CHAIN 85 1447
FT INIT MET 85 85
FT DOMAIN 26 1097
FT TRANSMEM 1098 1122
FT DOMAIN 1123 1447
FT DOMAIN 36 135
FT DOMAIN 139 229
FT DOMAIN 234 326
FT DOMAIN 331 416
FT DOMAIN 426 522
FT DOMAIN 525 618
FT DOMAIN 619 716
FT DOMAIN 722 816
FT DOMAIN 840 940
FT DOMAIN 941 1042
FT DISULFID 61 117
FT DISULFID 161 212
FT DISULFID 261 310
FT DISULFID 352 400
FT CARBOHYD 60 60
FT CARBOHYD 94 94
FT CARBOHYD 299 299
FT CARBOHYD 318 318
FT CARBOHYD 478 478
FT CARBOHYD 628 628
FT CARBOHYD 702 702
FT VARSPLIC 819 838
FT
FT
SQ SEQUENCE 1447 AA; 158298 MW; 0D1F1097C22D5B9F CRC64;

Query Match 13.0%; Score 209; DB 1; Length 1447;
Best Local Similarity 27.7%; Pred. No. 3.6e-08;
Matches 67; Conservative 37; Mismatches 98; Indels. 40; Gaps 10;

Qy 51 MSCRASGPPPTIEMLINGOPLSMVPPDPH-HLAPDGTLL--LQPPARGHAHDCQALST 107
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 LKCEVIGEPMTIHWQRKQDLNPLPGDSRVVLPFGALQISRLQP-----G 205
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 108 DLGVVTCASNRGLTAVSRGARLSVAVLRD-----FQIQRDMVAVVGEQFTLECGP 160
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 DSGVYRCSARN--PASITGNEAEVRILSDPGLHRLQYFLQRPNSVIAIEGKDAVLECCV 263
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 161 PWGHPPTVSWWKDGKPLALQGRHTVSGGS-LLMARAEKSDXTYMCVATNSAGHRER 219
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 264 S-GYPPSPFTWLGRGEVIQLRSKKYSLGGSNLLISNVTDDSGTTCVVTYKNNISAS 322
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 220 AARVSIQEPQDYTPVELLA---VRIQLENTVLTNPDPAPGPKPAPVWLXKVGSPXRL 276
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 323 AELTVLPVFPFLNPLNSLYAYESMDIEFE-----CAVSGKPVPTV--NWMKNGDVVI 372
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 277 PN 278
| :
Db 373 PS 374

RESULT 14
NRG_DROME
ID NRG_DROME STANDARD; PRT; 1302 AA.
AC P20241; O61541; O61542; Q24414; Q24415; Q95U64; Q9V3X0;
DT 01-FEB-1991 (Rel. 17, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
```



DE Neuroglial precursor.  
GN NRG OR CGI634.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND SEQUENCE OF 24-41 AND 737-751.  
RX MEDLINE=90030418; PubMed=2805067;  
RA Bieber A.J., Snow P.M., Hortsch M., Patel N.H., Jacobs J.R.,  
RA Traquina Z.R., Schilling J., Goodman C.S.;  
RT "Drosophila neuroglial: a member of the immunoglobulin superfamily  
RT with extensive homology to the vertebrate neural adhesion molecule  
RT L1";  
RL Cell 59:447-460(1989).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=98332718; PubMed=9666073;  
RA Zhao G., Hortsch M.;  
RT "The analysis of genomic structures in the L1 family of cell adhesion  
RT proteins provides no evidence for exon shuffling events after the  
RT separation of arthropod and chordate lineages.";  
RL Gene 215:47-55(1998).  
RN [3]  
RP REVISIONS.  
RA Hortsch M.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX STRAIN=Berkely;  
RC MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Burtis K.C., Rogers Y.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX STRAIN=Berkely; TISSUE=Head;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.B., Rubin G.M., Celniker S.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 1182-1302 FROM N.A., FUNCTION, ALTERNATIVE SPLICING, AND  
RP TISSUE SPECIFICITY.  
RX MEDLINE=90262720; PubMed=1693086;  
RA Hortsch M., Bieber A.J., Patel N.H., Goodman C.S.;  
RT "Differential splicing generates a nervous system-specific form of  
RT Drosophila neuroglial";  
RL Neuron 4:697-703(1990).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 610-814.  
RX MEDLINE=94213741; PubMed=7512815;  
RA Huber A.H., Wang Y.-M.E., Bieber A.J., Bjorkman P.J.;  
RT "Crystal structure of tandem type III fibronectin domains from  
RT Drosophila neuroglial at 2.0 A.";  
RL Neuron 12:717-731(1994).  
RN [8]  
RP -1- FUNCTION: THE LONG ISOFORM MAY PLAY A ROLE IN NEURAL AND GLIAL  
RP CELL ADHESION IN THE DEVELOPING EMBRYO. THE SHORT ISOFORM MAY BE A  
RP MORE GENERAL CELL ADHESION MOLECULE INVOLVED IN OTHER TISSUES AND  
RP IMAGINAL DISK MORPHOGENESIS. VITAL FOR EMBRYONIC DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=P20241-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P20241-2; Sequence=VSP\_002601\_VSP\_002602;  
CC -1- TISSUE SPECIFICITY: LONG ISOFORM IS RESTRICTED TO SURFACE OF  
CC NEURONS AND GLIA IN THE DEVELOPING NERVOUS SYSTEM AND THE SHORT  
CC ISOFORM TO OTHER NONNEURAL TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -1- SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.  
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
CC  
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CC  
CC -----  
CC EMBL; M28231; AAA28728.2; -;  
CC EMBL; AF050085; AAC28613.2; -;  
CC EMBL; AF050084; AAC28613.2; JOINED.  
CC EMBL; AF050085; AAC28614.2; -;  
CC EMBL; AF050084; AAC28614.2; JOINED.  
CC EMBL; AF003444; AAF46387.1; -;  
CC EMBL; AY058284; AAL13513.1; -;  
CC EMBL; X76243; CAA53822.1; -;  
CC EMBL; X76244; CAA53823.1; -;  
CC PDB; 1CFB; 30-NOV-94.  
CC FlyBase; FBgn0002968; Nrg.  
CC GO; GO:0005886; C:plasma membrane; IEP.  
CC GO; GO:0005194; F:cell adhesion molecule activity; IMP.  
CC GO; GO:0007560; P:imaginal disc morphogenesis; IMP.  
CC GO; GO:0007158; P:neutrophil cell adhesion; IMP.  
CC InterPro; IPR003961; FN.III.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003598; Ig\_C2.  
CC Pfam; PF00041; fn3; 5.  
CC Pfam; PF00047; ig; 6.  
CC SMART; SM00408; IGC2; 4.  
CC SMART; SM00060; FN3; 5.  
CC PROSITE; PS00835; IG\_LIKE; 6.  
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; 3D-structure;





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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:51:24 ; Search time 31.9223 Seconds  
(without alignments)  
2449.385 Million cell updates/sec

Title: US-10-047-021-86  
Perfect score: 1608  
Sequence: 1 MGSGGDSILGGRGSLPLLLL.....SGPLPREARELRQRRNTG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organalle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1444	89.8	1007	4 Q8WZ75	Q8WZ75 homo sapien
2	1436	89.3	792	4 Q96JV6	Q96JV6 homo sapien
3	1112.5	69.2	1016	11 Q8C310	Q8C310 mus musculus
4	791	49.2	702	4 Q8TEG1	Q8TEG1 homo sapien
5	452.5	28.1	1034	4 Q96MS0	Q96MS0 homo sapien
6	448.5	27.9	1651	11 Q55005	Q55005 rattus norv
7	446.5	27.8	1651	4 Q916N7	Q916N7 homo sapien
8	445.5	27.7	1612	11 Q89026	Q89026 mus musculus
9	444.5	27.6	330	13 Q90242	Q90242 gallus gall
10	432	26.9	1614	13 Q8UV7	Q8UV7 xenopus lae
11	423	26.3	1513	13 Q90270	Q90270 brachydanio
12	414.5	25.8	1344	11 Q92214	Q92214 mus musculus
13	407	25.3	333	13 Q90241	Q90241 gallus gall
14	406	25.2	1419	13 Q98SW3	Q98SW3 brachydanio
15	405	25.2	1389	13 Q90269	Q90269 brachydanio
16	405	25.2	1395	5 Q9W213	Q9W213 drosophila

17	405	25.2	1395	5	O44924	O44924 drosophila
18	404.5	25.2	1380	4	O9HCK4	O9HCK4 homo sapien
19	400.5	24.9	1675	13	Q98SW4	Q98SW4 brachydanio
20	398.5	24.8	227	11	Q8BJ59	Q8BJ59 mus musculus
21	397.5	24.7	1342	5	Q9GPP6	Q9GPP6 drosophila
22	397.5	24.7	1342	5	Q9VP27	Q9VP27 drosophila
23	360	22.4	1269	5	O01632	O01632 caenorhabdi
24	360	22.4	1273	5	O44928	O44928 caenorhabdi
25	358	22.3	1406	5	Q9GPP7	Q9GPP7 drosophila
26	358	22.3	1463	5	Q9VQ08	Q9VQ08 drosophila
27	351	21.8	1060	11	Q9QZ13	Q9QZ13 rattus norv
28	348.5	21.7	376	13	Q90271	Q90271 brachydanio
29	267.5	16.6	1496	4	Q92626	Q92626 homo sapien
30	261.5	16.3	1151	11	Q9QVN5	Q9QVN5 rattus sp.
31	261.5	16.3	1174	11	Q91260	Q91260 rattus norv
32	261.5	16.3	1217	11	P97685	P97685 rattus norv
33	260.5	16.2	298	4	Q96HT1	Q96HT1 homo sapien
34	260.5	16.2	1028	11	P97528	P97528 rattus norv
35	260.5	16.2	1041	4	O94856	O94856 homo sapien
36	259	16.1	1311	5	O961K8	O961K8 drosophila
37	259	16.1	1527	5	Q9VZ24	Q9VZ24 drosophila
38	258.5	16.1	1898	11	Q9EQ17	Q9EQ17 mus musculus
39	254.5	15.8	1948	4	Q13332	Q13332 homo sapien
40	254	15.8	498	11	Q8BET6	Q8BET6 mus musculus
41	254	15.8	705	11	Q8CBD3	Q8CBD3 mus musculus
42	253.5	15.8	814	4	Q81VU1	Q81VU1 homo sapien
43	253.5	15.8	1898	11	Q64604	Q64604 x protein-t
44	253	15.7	1535	5	Q23991	Q23991 drosophila
45	252.5	15.7	1028	11	Q8C6X1	Q8C6X1 mus musculus

#### ALIGNMENTS

#### RESULT 1

Q8WZ75	PRELIMINARY;	PRT; 1007 AA.
ID	Q8WZ75	
AC	Q8WZ75;	
DT	01-MAR-2002 (Tremblrel. 20, Created)	
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)	
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)	
DE	Magic roundabout.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_taxid=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20530916; PubMed=11076864;	
RA	Huminiecki L., Bicknell R.;	
RT	"In silico cloning of novel endothelial-specific genes.";	
RL	Genome Res. 10:1796-1806(2000).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	Huminiecki L., Bicknell R.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF361473; AAL31867.1;	
DR	GeneW; HGNC:17985; ROBO4.	
DR	InterPro; IPR003961; FN III.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003598; IG_c2.	
DR	InterPro; IPR003006; IG_MHC.	
DR	Pfam; PF00041; fn3; 2.	
DR	Pfam; PF00047; ig; 2.	
DR	SMART; SM00060; FN3; 2.	
DR	SMART; SM00408; IGC2; 1.	
DR	PROSITE; PS50835; IG_LIKE; 2.	
KW	Immunoglobulin domain.	
SQ	SEQUENCE 1007 AA; 107457 MW; E43F246CS9BE1415 CRC64;	

Query Match 89.8%; Score 1444; DB 4; Length 1007;  
Best Local Similarity 98.9%; Pred. No. 2.6e-115;  
Matches 270; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MGSGLDILGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 60
DB 1 MGSGLDILGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 60
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
DB 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
QY 121 GTAVSRGARLSVAVLRDFOQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
DB 121 GTAVSRGARLSVAVLRDFOQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
QY 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQBPQDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQBPQDYTEPVELLAV 240
QY 241 RIQLENTVTLNPDPAEGPKPRPAVWLXWKVSGP 273
DB 241 RIQLENTVTLNPDPAEGPKPRPAVWLXWKVSGP 273
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## RESULT 2

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Q96JV6 ID Q96JV6 PRELIMINARY; PRT; 792 AA.
AC Q96JV6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein FJ114946.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isoqai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Foglia S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027852; BAB5411.1;
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_Like; 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 792 AA; 85419 MW; FC6DC05275B7B234 CRC64;
```

```
Query Match 89.3%; Score 1436; DB 4; Length 792;
Best Local Similarity 98.5%; Pred. No. 9.5e-115;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSGLDILGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 60
DB 1 MGSGLDILGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 60
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
DB 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
QY 121 GTAVSRGARLSVAVLRDFOQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
DB 121 GTAVSRGARLSVAVLRDFOQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLAL 180
```

```
QY 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQBPQDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQBPQDYTEPVELLAV 240
QY 241 RIQLENTVTLNPDPAEGPKPRPAVWLXWKVSGP 273
DB 241 RIQLENTVTLNPDPAEGPKPRPAVWLXWKVSGP 273

RESULT 3
Q8C310 ID Q8C310 PRELIMINARY; PRT; 1016 AA.
AC Q8C310;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to MAGIC ROUNDABOUT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK087355; BAC39850.1;
SQ SEQUENCE 1016 AA; 108461 MW; DE70683C63AECDE8E CRC64;
```

```
Query Match 69.2%; Score 1112.5; DB 11; Length 1016;
Best Local Similarity 77.4%; Pred. No. 7.6e-87;
Matches 212; Conservative 20; Mismatches 41; Indels 1; Gaps 1;

QY 1 MGSGLDILGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 60
DB 11 MGSGLDILGGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFOGPGPARMSCRASGQPP 70
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQ-ALSTDLGVYTCEASNRL 119
DB 71 PTIRWLLNGQPLSMVPPDPHLLPDGTLTLLHRSVQGRPDQDQNILSAILGVYTCEASNRL 130
QY 120 LGTAVSRGARLSVAVLRDFOQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLA 179
DB 131 LGTAVSRGARLSVAVLRDFOQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLV 190
QY 180 LQGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQBPQDYTEPVELLA 239
DB 191 LQGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQBPQDYTEPVELLA 250
QY 240 VRIQLENTVTLNPDPAEGPKPRPAVWLXWKVSGP 273
DB 251 VRIQLENTVTLNPDPAEGPKPRPAVWLXWKVSGP 284

RESULT 4
Q8TEG1 ID Q8TEG1 PRELIMINARY; PRT; 702 AA.
AC Q8TEG1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FLJ00236 protein (Fragment).
GN FLJ00236.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

RC TISSUE=Spleen;  
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;  
RT "The nucleotide sequence of a long cDNA clone isolated from human  
spleen."  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK074163; BAB84989.1; -  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00060; FN3; 2.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Immunoglobulin domain  
FT NON TER 1  
SQ SEQUENCE 702 AA; 75340 MW; D668FEE4BCAFDCC6 CRC64;  
  
Query Match 49.2%; Score 791; DB 4; Length 702;  
Best Local Similarity 59.0%; Pred. No. 1.9e-59;  
Matches 161; Conservative 0; Mismatches 2; Indels 110; Gaps 1;  
  
QY 1 MSGGDSLLGGRGSLPLLLIMGMAQDSPQILVHPQDQLFQGGPARMSCRSGQPP 60  
DB 1 MSGGDSLLGGRGSLPLLLIM----- 23  
  
QY 61 PTIRWLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEASNRL 120  
DB 24 ----- 23  
  
QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVGGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180  
DB 24 -----VLREDFQIQPRDMVAVGGEQFTLECGPPWGHPEPTVSWKDGKPLAL 70  
  
QY 181 QGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240  
DB 71 QGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 130  
  
QY 241 RIQLENTVLLNPDPAEGKPRPAVWLXWVSGP 273  
DB 131 RIQLENTVLLNPDPAEGKPRPAVWLXWVSGP 163  
  
RESULT 5  
Q96MS0 PRELIMINARY; PRT; 1034 AA.  
AC Q96MS0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ31982.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,  
Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,  
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
Matsuoka K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,  
Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K., Isogai T.;  
RT "NEDO human cDNA sequencing project."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK056544; BAB71212.1; -  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.

DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; ig; 5.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00408; IGC2; 5.  
DR PROSITE; PS0835; IG LIKE; 5.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 1034 AA; 110723 MW; 09E13C7B424F7E30 CRC64;  
  
Query Match 28.1%; Score 452.5; DB 4; Length 1034;  
Best Local Similarity 40.7%; Pred. No. 3.5e-30;  
Matches 118; Conservative 27; Mismatches 104; Indels 41; Gaps 10;  
  
QY 1 MSGGDSLLGGRGSLPLLLIMGMA-----QDSPQILVHPQDQLFQGGPAR 50  
DB 23 ISNSSELLGFNSSLAALNHTLLPPGDPSLNGSRVGPEDAMPRIQEPDILLVSRGEPAT 82  
  
QY 51 MSCRASQPPPTIRWLNGQPLSMVPPDP--HH-LLPDGTLTLLQPPARGHAHQALST 107  
DB 83 LPCRAEGRPRNIEWYKNGARVATVREDPRAHRLLLPSGALFF--PRIVH--GRRARP 136  
  
QY 108 DLGVYTCEASNRLCTAVSRGARLSVAVLRDFQIQPRDMVAVGGEQFTLECGPPWGHPEP 167  
DB 137 DEGVYTCVARNYLGAASRNASLEAVLRDDFQSPGNVVAVGEPVAVLECVPRGHPPEP 196  
  
QY 168 TVSWKDGKPLAQPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQ 227  
DB 197 SVSWKDGARLKEBEGRTITGGKLMWSHTLKS DAGMYVCVASNAGERESAAAEVVMVLE 256  
  
QY 228 -PDYTEPVELLAVRIQLENTVLLNPDPAE-----GPKRPPAVWLXWK 269  
DB 257 RPSFLRPV-----NQVVLADAPVTLCEVKGDPDPPR----LRWR 292  
  
RESULT 6  
O55005 PRELIMINARY; PRT; 1651 AA.  
AC O55005;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Transmembrane receptor Robol.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spinal cord;  
RX MEDLINE=98117249; PubMed=9458045;  
RA Klad T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,  
Goodman C.S., Tear G.  
RT "Roundabout controls axon crossing of the CNS midline and defines a  
novel subfamily of evolutionarily conserved guidance receptors."  
RL Cell 92:205-215 (1998).  
DR EMBL; AF041082; AAC39960.1; -  
DR HSSP; P56276; 1TLK.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; ig; 5.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00408; IGC2; 5.  
DR PROSITE; PS0835; IG LIKE; 5.  
KW Immunoglobulin domain; Receptor.  
SQ SEQUENCE 1651 AA; 180747 MW; FA2452DD46E186B7 CRC64;  
  
Query Match 27.9%; Score 448.5; DB 11; Length 1651;  
Best Local Similarity 42.2%; Pred. No. 1.4e-29;  
Matches 92; Conservative 31; Mismatches 86; Indels 9; Gaps 2;  
  
QY 28 QDSPQILVHPQDQLFQGGPARMSCRSGQPPPTIRWLNGQPLSMVPPDPH----LLP 84

Db 64 EDFPRIVEHPSDLIVSGEPATLNCRAEGRPPTTIEWYKGERVETDKDDPRSHRMLLP 123  
Qy 85 DGTLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFOIQPR 144  
Db 124 SGSLFFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVAAILRDDFRQNP 177  
Qy 145 DMVAVGQFTLECGPPWGHPEPTVSWWKGKPLALQGRHTVSGGSLMARAEKSDXT 204  
Db 178 DMVAVGEPVMEQPPRGHPEPTISWKGKPLALQGRHTVSGGSLMARAEKSDXT 237  
Qy 205 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242  
Db 238 YVCVTNMVGERSEVAELTVLERPSFVKRPSNLAATV 275

## RESULT 7

Q9Y6N7 PRELIMINARY; PRT; 1651 AA.  
AC Q9Y6N7;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Roundabout 1.  
GN ROBO1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98117249; PubMed=9458045;  
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,  
RA Goodman C.S., Tear G.;  
RT "Roundabout controls axon crossing of the CNS midline and defines a  
RT novel subfamily of evolutionarily conserved guidance receptors.";  
RL Cell 92:205-215(1998).  
DR EMBL; AF040990; AAC39575.1; -.  
DR HSSP; P56276; ITLK.  
DR Genew; HGNC:10249; ROBO1.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; ig; 5.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
SQ SEQUENCE 1651 AA; 180929 MW; 9D98CD7CAB73074D CRC64;

Query Match 27.8%; Score 446.5; DB 4; Length 1651;  
Best Local Similarity 41.7%; Pred. No. 2e-29;  
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 28 QDSPPOILVHPDOLFCQPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHH---LLP 84  
Db 64 EDFPRIVEHPSDLIVSGEPATLNCRAEGRPPTTIEWYKGERVETDKDDPRSHRMLLP 123  
Qy 85 DGTLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFOIQPR 144  
Db 124 SGSLFFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVAAILRDDFRQNP 177  
Qy 145 DMVAVGQFTLECGPPWGHPEPTVSWWKGKPLALQGRHTVSGGSLMARAEKSDXT 204  
Db 178 DMVAVGEPVMEQPPRGHPEPTISWKGKPLALQGRHTVSGGSLMARAEKSDXT 237  
Qy 205 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242  
Db 238 YVCVTNMVGERSEVAELTVLERPSFVKRPSNLAATV 275

## RESULT 8

O89026 PRELIMINARY; PRT; 1612 AA.  
ID O89026;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Dutt1 protein.  
GN ROBO1 OR DUTT1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Wu M.C., Lowe N., Fordham R., Rabbitts P.;  
RT "The mouse homologue of human DUTT1/H-robol gene: protein sequence and  
RT chromosomal location.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y17793; CAA76850.1; -.  
DR HSSP; P56276; ITLK.  
DR MGD; MGI:1274781; Robol.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; ig; 5.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
SQ SEQUENCE 1612 AA; 176406 MW; 5F2988C544796B4B CRC64;

Query Match 27.7%; Score 445.5; DB 11; Length 1612;  
Best Local Similarity 41.7%; Pred. No. 2.4e-29;  
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 28 QDSPPOILVHPDOLFCQPGPARMSCRASGPPPTIRWLLNGQPLSMVPPDPHH---LLP 84  
Db 25 EDFPRIVEHPSDLIVSGEPATLNCRAEGRPPTTIEWYKGERVETDKDDPRSHRMLLP 84  
Qy 85 DGTLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLREDFOIQPR 144  
Db 85 SGSLFFLR-----IVHGKSRPDEGVYICVARNYLGEAVSHNASLEVAAILRDDFRQNP 138  
Qy 145 DMVAVGQFTLECGPPWGHPEPTVSWWKGKPLALQGRHTVSGGSLMARAEKSDXT 204  
Db 139 DMVAVGEPVMEQPPRGHPEPTISWKGKPLALQGRHTVSGGSLMARAEKSDXT 198  
Qy 205 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 242  
Db 199 YVCVTNMVGERSEVAELTVLERPSFVKRPSNLAATV 236

## RESULT 9

Q90242 PRELIMINARY; PRT; 330 AA.  
ID Q90242;  
AC Q90242;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Roundabout1 protein (fragment).  
GN ROBO1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21366016; PubMed=11472852;  
RA Vargesson N., Luria V., Messina I., Erskine L., Laufer E.;  
RT "Expression patterns of Slit and Robo family members during vertebrate



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limb development."
RL Mech. Dev. 106:175-180(2001).
DR EMBL; AF364047; AAK94293.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
FT NON_TER 1
FT SEQUENCE 330 AA; 36725 MW; 0613488F78CBE61 CRC64;
SQ
Query Match 27.6%; Score 444.5; DB 13; Length 330;
Best Local Similarity 40.9%; Pred. No. 4.1e-30;
Matches 94; Conservative 32; Mismatches 93; Indels 11; Gaps 3;
QY 18 LLLIMGG--NAQDSPQILVHPDQLFGPGPARMSCRAGQPPTIRWLLNGQPLSMV 75
DB 7 LLCLASGSLRQEDFPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIETWYKGGERVETD 66
QY 76 PDPDH---LIPDGTLLQLPPARGHADGQALSTDLGVYTCASNRLGTAVSRGARLSV 132
DB 67 KDDPRSHRMLLPSSGLFFLR-----IVHGRKSRDEGVYVCVARNYLGEAVSHNASLEV 120
QY 133 AVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWMKDGKPLALQPGRHTVSGGSL 192
DB 121 AILRDDFRQNSDVMVAVGEPAVMCEQPRGHPEPTISWKKGDTPIDDDKDERITIRGGKL 180
QY 193 LMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPDQYTFPEVLLAVRI 242
DB 181 MITTRKNDAGKYCVGCTNMVGERSEVAELTVLERPSFLRPSNNAVTV 230
RESULT 10
Q8UVD7 PRELIMINARY; PRT; 1614 AA.
AC Q8UVD7;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Roundabout-1.
GN ROBO1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Connor R.M., Key B.;
RT "Dual role for Roundabout-1 in neural differentiation and axon
pathfinding in the Xenopus forebrain."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461119; AAL66361.1; -.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
KW PROSITE; PS50835; IG LIKE; 5.
KW Immunoglobulin domain.
SQ SEQUENCE 1614 AA; 176733 MW; 01D2C3D6593F3935 CRC64;
Query Match 26.9%; Score 432; DB 13; Length 1614;
Best Local Similarity 40.6%; Pred. No. 3.5e-28;
Matches 89; Conservative 32; Mismatches 88; Indels 10; Gaps 3;
QY 28 QDSPQILVHPDQLFGPGPARMSCRAGQPPTIRWLLNGQPLSMVPPDPHH---LLP 84
limb development."
RL Mech. Dev. 106:175-180(2001).
DR EMBL; AF364047; AAK94293.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
FT NON_TER 1
FT SEQUENCE 330 AA; 36725 MW; 0613488F78CBE61 CRC64;
SQ
Query Match 27.6%; Score 444.5; DB 13; Length 330;
Best Local Similarity 40.9%; Pred. No. 4.1e-30;
Matches 94; Conservative 32; Mismatches 93; Indels 11; Gaps 3;
QY 18 LLLIMGG--NAQDSPQILVHPDQLFGPGPARMSCRAGQPPTIRWLLNGQPLSMV 75
DB 7 LLCLASGSLRQEDFPRIVEHPSDLIVSKGEPATLNCKAEGRPPTIETWYKGGERVETD 66
QY 76 PDPDH---LIPDGTLLQLPPARGHADGQALSTDLGVYTCASNRLGTAVSRGARLSV 132
DB 67 KDDPRSHRMLLPSSGLFFLR-----IVHGRKSRDEGVYVCVARNYLGEAVSHNASLEV 120
QY 133 AVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWMKDGKPLALQPGRHTVSGGSL 192
DB 121 AILRDDFRQNSDVMVAVGEPAVMCEQPRGHPEPTISWKKGDTPIDDDKDERITIRGGKL 180
QY 193 LMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPDQYTFPEVLLAVRI 242
DB 181 MITTRKNDAGKYCVGCTNMVGERSEVAELTVLERPSFLRPSNNAVTV 230
RESULT 11
Q90Z70 PRELIMINARY; PRT; 1513 AA.
AC Q90Z70;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Roundabout2.
GN ROBO2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.S., Ray R., Chien C.B.;
RT "Cloning and expression of three zebrafish roundabout homologs suggest
roles in axon guidance and cell migration."
RL Dev. Dyn. 221:216-230(2001).
DR EMBL; AF337035; AAK58427.1; -.
DR ZFIN; ZDB-GENE-001019-1; robo2.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50835; IG LIKE; 5.
KW Immunoglobulin domain.
SQ SEQUENCE 1513 AA; 165181 MW; D1743BACCC089F0 CRC64;
Query Match 26.3%; Score 423; DB 13; Length 1513;
Best Local Similarity 35.1%; Pred. No. 1.9e-27;
Matches 97; Conservative 40; Mismatches 97; Indels 42; Gaps 7;
QY 16 PLLLLLLMGH-----AQSPPQILVHPDQLFGPGPARMSCRAGQPPTIR 64
DB 3 PLTHLLCGLVYFNQVDSRLRQEDSPRIVEHPSDLIVSKGEPATLNCKAEGRPPTVE 62
QY 65 WLLNGQPLSMVPPDPHH---LLPDGTLLQLPPARGHADGQALSTDLGVYTCASNRLG 121
DB 63 WKDGERVETDKDPRSHRMLLPSSGLFFLR-----IVHGRKSRDEGVYVCVARNYL 116
QY 122 TAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWMKDGKPLAQ 181
DB 117 EAVSRNASLEVALLRDDFRQNPDTVVAAGSPAILECVPRGHPEPTIYWKDKVRIDEK 176
QY 182 PGRHTVSGGSLMARAEKSDXTYMCVATNSAGHRESRAARVSI-QEPDQYTFV----- 235
DB 177 DDRIKIRGGKLMINTRKSDAGMVICVGTNMVGERDSETAQVTFVFERPTFLRRPTNQVL 236

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Qy 236 --ELLAVRIQLENTLLNPDPAEGKPRPAVLXWK 269
      | | | | | | | | | | | | | | | | | |
Db 237 BEEAVERFCVQG-----DQPS-----IRWK 258

RESULT 12
ID Q92214 PRELIMINARY; PRT; 1344 AA.
AC Q92214;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rig-1 protein.
GN RBIG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RP SEQUENCE FROM N.A.
RA Yuan S.-S.F., Cox L.A., Dasika G.K., Lee E.Y.-H.P.;
RL Submitted (APR-1998) to the ENBL/GenBank/DBJ databases.
DR EMBL; AF060570; AAD11628.1; -.
DR HSSP; P56276; IRLK.
DR MGD; MGI:1343102; RBIG1.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Immunoglobulin domain.
SQ SEQUENCE 1344 AA; 143439 MW; 8B0060341C49CFEA CRC64;

Query Match 25.8%; Score 414.5; DB 11; Length 1344;
Best Local Similarity 39.9%; Pred. No. 8.9e-27;
Matches 101; Conservative 27; Mismatches 94; Indels 31; Gaps 8;

Qy 28 QDSPQILVHPDQOLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDP--HH-LLP 84
      | | | | | | | | | | | | | | | | | |
Db 38 EDAMPRIVEQPDLVSRGEPATLPCRAEGRPENIEWYKNGARVATAREDPRAHRLLP 97

Qy 85 DGTLLLOPPARGAHDCQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDFQIQPR 144
      | | | | | | | | | | | | | | | | | |
Db 98 SGALFF---PRVH---GRRSRPDEGVYTCVARNYLGAASRNASLEAVLRLDDFQSPG 151

Qy 145 DMVAVVGQFTLECGPPMGHPPTVSWWKGKPLALOPGRHTVSGSLLMARAESKDEXT 204
      | | | | | | | | | | | | | | | | | |
Db 152 NVVAVGEPVAVMECVPPKGPHEPLVWTKGKIKLKEBEGRTIRGGKLMWSTTKSDAGM 211

Qy 205 YMCVATNSAGHRESRAAR-VSIQEPQDYTEPVELLAVRIQLENTLLNPDPAE----- 256
      | | | | | | | | | | | | | | | | | |
Db 212 YMCVASNMAGRESGAELVLERPSFLRRP-----NQVLADAPVNFCEVQG 261

Qy 257 GPKPRPAVLXWK 269
      | | | | | | | |
Db 262 DPQPN-----LHW 270

RESULT 13
Q90241 PRELIMINARY; PRT; 333 AA.
ID Q90241;
AC Q90241;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Roundabout2 protein (Fragment).
GN ROBO2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2004, 12:28:30 ; Search time 1838.41 Seconds  
(without alignments)  
4005.776 Million cell updates/sec

Title: US-10-047-021-86  
Perfect score: 1608  
Sequence: 1 MGSGDLSLGGSGSLPLLL.....SGPRLPREARELRQRRNTG 303

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-Q=/cgn2\_1/USPTO\_spool\_p/US10047021/runat\_30012004\_145453\_24574/app\_query.fasta\_1.910  
-MODEL=frame+p2n.model -DEV=xlp  
-DB=E8T -QFMT=fastap -SUFFIX=rat -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10047021 @CGN 1.1 4399 @runat\_30012004\_145453\_24574 -NCPU=3  
-NO WMAP -LARGEQUERY -NEG-TIMEOUT=30 -WAIT -DSPBLOCK=100 -LONLOG  
-DEV\_TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hcc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hcc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1565	97.3	3758	11	BC039602	BC039602 Homo sapi
2	1520	94.5	1201	9	AL553360	AL553360 AL553360
3	1345	83.6	1019	12	BM921911	BM921911 AGENCOURT
4	1265	78.7	922	13	BX418142	BX418142 BX418142
5	1234	76.7	826	14	CB994099	CB994099 AGENCOURT
6	1214.5	75.5	860	14	CB996189	CB996189 AGENCOURT
7	1146.5	71.3	941	13	BQ890126	BQ890126 AGENCOURT
8	1145.5	71.2	3689	11	AK004723	AK004723 Mus muscu
9	1145.5	71.2	3865	11	AK087355	AK087355 Mus muscu
10	1135.5	70.6	803	14	CB997292	CB997292 AGENCOURT
11	1112	69.2	729	12	BI762862	BI762862 603048384
12	1030	64.1	1230	12	BM906521	BM906521 AGENCOURT
13	1025.5	63.8	771	14	CB959649	CB959649 AGENCOURT
14	1017	63.2	798	14	CB961529	CB961529 AGENCOURT
15	980	60.9	688	14	CB961818	CB961818 AGENCOURT
16	967	60.1	797	14	CB961002	CB961002 AGENCOURT
17	936	58.2	558	9	AL602474	AL602474 DKFZp6860
18	920	57.2	1087	12	BM914311	BM914311 AGENCOURT
19	891.5	55.4	610	10	BG745318	BG745318 60723637
20	865	53.8	502	13	BX474842	BX474842 DKFZp686M
21	863	53.7	570	10	BE233526	BE233526 139756 MA
22	825.5	51.3	662	14	BY727209	BY727209 BY727209
23	789	49.1	532	13	BX475138	BX475138 DKFZp6860
24	787.5	49.0	620	10	BB664621	BB664621 BB664621
25	784	48.8	526	14	CA394658	CA394658 c954c07.Y
26	775	48.2	501	13	BX474746	BX474746 DKFZp686B
27	730.5	45.4	631	10	BE376779	BE376779 601227331
28	700	43.5	438	13	BX475177	BX475177 DKFZp686F
29	660.5	41.1	529	4	BX520802	BX520802 RZPD Mus
30	660	41.0	424	13	BX475172	BX475172 DKFZp686E
31	660	41.0	426	2	MSM085795	Bx492967 Homo sapi
32	659.5	41.0	551	9	AI116483	AI116483 ud74c06.Y
33	657.5	40.9	557	14	BY704924	BY704924 BY704924
34	585.5	36.4	1257	14	CB993951	CB993951 AGENCOURT
35	574	35.7	344	9	AA577940	AA577940 nl20d01.s
36	572.5	35.6	455	10	BB839755	BB839755 BB839755
37	566	35.2	450	9	AL039859	AL039859 DKFZp434E
38	541	33.6	555	12	BI836220	BI836220 603085778
39	529	32.9	532	12	BI159602	BI159602 602920006
40	507.5	31.6	444	13	BY270114	BY270114 BY270114
41	486.5	30.3	441	13	BY285423	BY285423 BY285423
42	476.5	29.6	379	10	BB871780	BB871780 BB871780
43	451	28.0	428	10	BB849408	BB849408 BB849408
44	439.5	27.3	414	13	BY268765	BY268765 BY268765
45	434.5	26.4	391	9	AA388861	AA388861 mp13e06.r

ALIGNMENTS

RESULT 1  
BC039602  
LOCUS BC039602 3758 bp mRNA linear HTC 06-NOV-2002  
DEFINITION Homo sapiens, Similar to roundabout homolog 4, magic roundabout  
(Drosophila), clone IMAGE:5590503, mRNA.  
ACCESSION BC039602  
VERSION BC039602.1 GI:24660430  
KEYWORDS HTC  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3758)

AUTHORS  
TITLE  
JOURNAL

Strausberg, R.  
Direct Submission  
Submitted (01-NOV-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgs.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Invitrogen  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
Contact: [amadane@systemsbio.org](mailto:amadane@systemsbio.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 84 Row: 1 Column: 5  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis, Genomescan gene prediction  
This clone has the following problem: frame shifted.

FEATURES  
source

Location/Qualifiers  
1..3758  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5590503"  
/tissue\_type="Ovary, pooled from 3 adults"  
/clone\_lib="NIH\_MGC\_125"  
/lab\_host="DH10B"  
/note="vector: pCMV-SPORT6"  
772 a 1232 c 1046 g 708 t

## Alignment Scores:

Pred. No.: 5.78e-107 Length: 3758  
Score: 1565.00 Matches: 295  
Percent Similarity: 98.67% Conservative: 1  
Best Local Similarity: 98.33% Mismatches: 3  
Query Match: 97.33% Indels: 1  
DB: 11 Gaps: 0

US-10-047-021-86 (1-303) x BC039602 (1-3758)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20  
Db 29 ATGGCTCTGGAGGAGACAGCCTCTGGGGGCGAGGGTTCCTGCTCTCTCTCTG 88  
Qy 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnLeuLeuValHisProGlnAsp 40  
Db 89 CTATCATGCGGAGGAGCATGGCTCAGGACTCCCGCCCGCCAGATCCTAGTCCACCCCGAGAC 148  
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
Db 149 CAGCTGTTCAGGGCCCTGGCCCTGCCAGGATGAGTGCCTCAAGCTCAGGCCACCCACCT 208  
Qy 61 ProThrLeuArgTTPLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80  
Db 209 CCCACCATCCCTGGTGTGTATGGGCGAGCCCTGAGCATGGTGGCCCGAGACCCACAC 268  
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
Db 269 CACCTCTCTGCTGATGGAGACCTTCTGCTGTACAGCCCTGCGCCGGGAGACATGCCAC 328  
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120  
Db 329 GATGCCAGGGCCCTGTCCACAGACTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 388  
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140

Db 389 GGCACGCGAGTCAGCAGAGGGCTCGCTGCTGTGGCTGTCTCCCGGAGATTCCAG 448  
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160  
Db 449 ATCCAGCCTCGGACATGCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 508  
Qy 161 ProTTPGlyHisProGluProThrValSerTrpTTPlyAspGlyLyProLeuAlaLeu 180  
Db 509 CCCTGGGGGCCACCCAGAGCCACAGTCTCATGTGTGGAAAGATGGGAAACCCCTGGCCCTC 568  
Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLySer 200  
Db 569 CAGCCCGGAGGACACAGTGTCCGGGGGGTCCCTGTGTGTGTGTGTGTGTGTGTGTGT 628  
Qy 201 AspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220  
Db 629 GACGAGGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCA 688  
Qy 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240  
Db 689 GCCCGGGTTCATCCAGGAGGCCCGCAGGACTACACGAGCCTGTGGAGCTTCTGGCTGTG 748  
Qy 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLyPro 260  
Db 749 CGAATTCAGCTGGAAATGTGACACTCTGAACCCGGATCTCGCAGAGGGCCCCAAGCCT 808  
Qy 261 ArgProAlaValTrpLeu\*\*\*TrpLyValSerGlyPro\*\*\*ArgLeuProAsnLeuTh 280  
Db 809 AGACCGCGGTGTGGCTCAGCTGGAGGTTCAGTGGGCCCTGTGGCCCTGCCCCAATCTTAC 868  
Qy 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
Db 869 ACGGCTTGTTCAGGACCCAGACTGCCCCGGAGGCGCAGGAGCTCCGTGGGCGAGAG 926

RESULT 2  
AL553360

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1..1201

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="CS01075Y13"

## /tissue\_type="PLACENTA COT 25-NORMALIZED"

## /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

## /notes="1st strand cDNA was primed with a NotI-oligo (dtr)

AL553360 1201 bp mRNA linear EST 31-MAY-2003  
AL553360 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
Clone CS01075Y13 5-PRIME, mRNA sequence.

AL553360  
GI:31275174

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12893123.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6206.r For

more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS01075CH07Q1&cluster=6206.r. Contact :

Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Paradise Avenue Genoscope sequence ID : CS01075CH07Q1.

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS01075Y13"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo (dtr)

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 236 a 348 c 369 g 212 t 36 others  
ORIGIN

## Alignment Scores:

Pred. No.: 3.5e-104 Length: 1201  
Score: 1520.00 Matches: 290  
Percent Similarity: 96.68% Conservative: 1  
Best Local Similarity: 96.35% Mismatches: 8  
Query Match: 94.53% Indels: 2  
DB: 9 Gaps: 0

US-10-047-021-86 (1-303) x AL553360 (1-1201)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20  
DB 81 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGGTTCTGCTGCTCTG 140  
QY 21 LeuileMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40  
DB 141 CTCATCATGGAGGATGCTCAGACTCCCGCCCGCATCTAGTCCACCCCGAGAC 200  
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
DB 201 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGATGAGTGCAGAGCTCCAGGCGGACCT 260  
QY 61 ProThrIleArgTrpLeuLeuGlnGlyGlnProLeuSerMetValProProAspProHis 80  
DB 261 CCCACATCCGCTGGTGTGTAATGGGAGCCCTGAGCATGGTGCCTCCAGACCCACAC 320  
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
DB 321 CACCTCTGCTGATGGAGACCTTCTGTGCTACAGCCCTGCGGGGAGATGCCACAC 380  
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120  
DB 381 GATGCCAGGCGCTGTCCACAGACTGGGTGTCTACATGTGAGCGACCAACGGGTT 440  
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140  
DB 441 GGCAGCGCATGTAGCAGAGCGCTCGGCTGTCTGTGCTGTCTCTCGGGAGATTTCAG 500  
QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160  
DB 501 ATCCAGCTCGGACATGCTGCTGTGTGGTGTAGCAGTTTACTCTGGAATGGGCGG 560  
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180  
DB 561 CCTGGGGCCACCCAGAGCCACAGTCTCATGTTGGAAAGATGGGAAACCCCTGGCCCTC 620  
QY 181 Gln-ProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysE 200  
DB 621 CACGCCCGGAGGACACATGCTCGGGGGGCTCTGCTGTGATGGCAAGCAGAGAGAG 680  
QY 200 rAspGlu\*\*\*ThrTrpMetCysValAlaAlaThrAsnSerAlaGlyHisArgGluSerArgAl 220  
DB 681 TGACAGAGGACCTACATGTGTGTGCTCCACCAACAGCGCAGGACATAGGAGAGCGGCG 740  
QY 220 alaArgValSerIleGlnGluProGlnAspTrpThrGluProValGluLeuAlaVala 240  
DB 741 ACCCGGGGTTTCATCCAGAGCCCGCAGGACTACACGAGCTGTGGAGCTTCTGGCTGT 800  
QY 240 InArgIleGlnLeuGluAenValThrLeuLeuAsnProAspProAlaGluGlyProLysPr 260  
DB 801 GCGAATTCAGCTGGAAATGTGACACTGCTGAACCCGGATCTCTCAGAGGGGCGCCCAAGCC 860  
QY 260 oArgProAlaValTrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeu 280  
DB 861 TAGACCGGGGTGTGGCTCAGCTGAGAGGTGAGTGGGCTGTGCGCTCGCCCAATCTTA 920  
QY 280 hrArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299

DB

RESULT 3

BM921911

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCES

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

CDNA

CDNA

CDNA

CDNA

CDNA

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Qy 95 AlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyValThrCys 114
Db 196 GCCGGGACATGCCACATGGCCAGCCCTGTCCACAGACCTGGGTGTCTACATGT 255
Qy 115 GluAlaSerAenArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
Db 256 GAGGCCAGCAACCGCTTGGCAGCGCAGTACAGCAGCGCTCGCTGTCTGTGGCTGTC 315
Qy 135 LeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValGlyGluGlnPhe 154
Db 316 CTCGGGAGGATTTCCAGATCAGCCTCGGACATGTGGTGTGGTGTGGTGTGGTGTGGT 375
Qy 155 ThrLeuGluCysGlyProProTyrGlyHisProGluProThrValSerTyrTyrLeuAsp 174
Db 376 ACTCTGGATGTGGCGCCCTTGGGCGCACCCAGGCCACAGTCTCATGTGGANAGAT 435
Qy 175 GlyIysProLeuAlaLeuGlnProGlyArgHisThrValSerGlySerLeuLeuMet 194
Db 436 GGGAAACCCCTGGCCCTCAGCCCGGAAGGACACAGTGTCCGGGGGCTCCTGTGTATG 495
Qy 195 AlaArgAlaGluIysSerAspGlu**ThrTyrMetCysValAlaThrAsnSerAlaGly 214
Db 496 GCAAGAGCAGAGAGAGAGTGCAGAGGACCTTACATGTGTGGCCACCAACAGCGCAGGA 555
Qy 215 HisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluPro 234
Db 556 CATGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCCGAGGACTACACGGAGCCT 615
Qy 235 ValGluLeuLeuAlaValArgIleGlnLeuGluAenValThrLeuLeuAenProAspPro 254
Db 616 GTGGAGCTTCTGGCTGTGCGAATTGAGCTGCGAATTTGAGCTGCTGCTGCTGCTGCT 675
Qy 255 AlaGluGlyProIysProArgProAlaValThrLeu**TyrIysValSerGlyPro*** 274
Db 676 GCAGAGGCCCGAAGCCTAGACCGCGGTGTGGCTCAGCTGGAANGTCAGTGGCCCTGCT 735
Qy 275 -ArgLeuProAenLeuThrArgProCysSerGlyProArgLeuProArg-GluAlaArg 293
Db 736 CGGCTGCCAATCTTACACGGCCCTTGTTCAGGACCCAGATGCCCCGGGAGGCCAGG 794

RESULT 4
BX418142 922 bp mRNA linear EST 13-MAY-2003
LOCUS BX418142 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF001Y124 5-PRIME, mRNA sequence.
ACCESSION BX418142
VERSION BX418142.1 GI:30642200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 922)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6206.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF001BE12Q1&cluster=6206.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DF001BE12Q1.
FEATURES
Location/Qualifiers
1..922
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone="CS0DF001Y124"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 189 a 286 c 277 g 158 t 12 others
ORIGIN
Alignment Scores:
Pred. No.: 3,31e-85 Length: 922
Score: 1265.00 Matches: 244
Percent Similarity: 97.21% Conservative: 0
Best Local Similarity: 97.21% Mismatches: 7
Query Match: 78.67% Indels: 1
DB: 13 Gaps: 0
US-10-047-021-86 (1-303) x BX418142 (1-922)
Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 170 ATGGGATCTGGAGGAGACAGCCTCTCGGGGGCAGGGGTTCCCTGCTCTGCTGCTG 229
Qy 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 230 CTATCATATGGAGGACATGGCTCAGGATYCCCGCCCCCAGATCTCTAGTCCACCC 289
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro 60
Db 290 CAGCTGTTCAGGGCCCTTGGCCCTCCAGGATGAGCTGCGGAGCTCAGGCCACG 349
Qy 61 ProThrIleArgTyrLeuLeuAenGlyGlnProLeuSerMetValProProAspPro 80
Db 350 CCCACCATCCGCTGGTTGCTGAAATGGGACGCCCTGAGCATGTGTGCCCCAGAC 409
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 410 CACCTCTGCTGTATGGGACCCCTTCTGCTGTCTACAGCCCTTGCCTCGGGGAC 469
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArg 120
Db 470 GATGCTCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCA 529
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPhe 140
Db 530 GGCACGGCAGTACAGAGCGCTCGGCTGTGTTGTGGCTGTCTCCGGGAGGATTTCC 589
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 160
Db 590 ATCCAGCCTCGGACATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 649
Qy 161 ProTyrGlyHisProGluProThrValSerTyrTyrIysAspGlyIysProLeuAla 180
Db 650 CCCTGGGGCCACCCAGAGCCCACTCTCATGTGTGGAAAGATGGGAAACCTGCTC 708
Qy 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGlySer 200
Db 709 CAGCCCGAAGGACACACAGTGTCCGGGGGATCCCTGTGTATGGCAGACAGAGAG 768
Qy 201 AspGlu**ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArg 220
Db 769 GACGAAGGAGCCTACATGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 828
Qy 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaVal 240
Db 829 SCCGGGGTTCATCCAGGAGCCCGAGGACTACACGGAGGCTGTGGAGCTTCTGG 888
Qy 241 ArgIleGlnLeuGluAenValThrLeuLeuAen 251
Db 889 CGAATACAGCTGGAAATGTGACACTGCTGAAC 921
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RESULT 5
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LOCUS
DEFINITION
AGENCOURT_13642710 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30331943 5', mRNA sequence.
ACCESSION
CB994099
VERSION
CB994099.1 GI:30288619
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 826)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM348 row: c column: 24
High quality sequence stop: 637.
Location/Qualifiers
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/clone="IMAGE:30331943"
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/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTTNN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NHGRI/NHGR)
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT 160 a 266 c 261 g 138 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 6,11e-83 Length: 826
Score: 1234.00 Matches: 243
Percent Similarity: 92.80% Conservative: 2
Best Local Similarity: 92.05% Mismatches: 14
Query Match: 76.74% Indels: 5
DB: 14 Gaps: 2
US-10-047-021-86 (1-303) x CB994099 (1-826)
QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 38 ATGGGCTCTGGAGGAGACAGCTCTCGGGGGGACGGGTTCCCTGCTGCTCTG 97
QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAsp 40
Db 98 CTCATCATGGAGGAGCATGCTCAGACTCCCGCCCGCCAGATCCTAGTCCACCCCGAGGAC 157
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro 60
Db 158 CAGCTGTTCCAGGGCCCTGGCCCTGCGCAGGATGAGTCCGAGCTCCAGGCCAGCCACT 217
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
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QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTrpCysGluAlaSerAsnArgLeu 120
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QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
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458 ATCCAGCTCGGGACATGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGGCGG 517
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
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CB996189
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DEFINITION
AGENCOURT_13622686 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30337143 5', mRNA sequence.
ACCESSION
CB996189
VERSION
CB996189.1 GI:30290709
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 860)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM361 row: 1 column: 16
High quality sequence stop: 578.
Location/Qualifiers

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Percent Similarity: 81.88% Conservatives: 3  
 Best Local Similarity: 80.87% Mismatches: 31  
 Query Match: 71.30% Indels: 24  
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US-10-047-021-86 (1-303) x B0890126 (1-941)

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 QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120  
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# RESULT 8

AK004723

LOCUS

DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200012D01 product:similar to MAGIC ROUNDABOUT [Homo sapiens], full insert sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
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 JOURNAL  
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 REFERENCE  
 AUTHORS

AK004723  
 GI:26334429  
 HTC; CAP trapper.  
 Mus musculus (house mouse)  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20499374  
 11042159

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakawa, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stauble, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wysshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S. and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
 21085660  
 11217851

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3689)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Horii, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

# TITLE JOURNAL

Submitted (10-JUL-2000) Yoshihide Hayaehizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

On Dec 10, 2002 this sequence version replaced gi:12836108.

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGCGAGCTCAATTAATTAATTAACCCGCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

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## CDS

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ORGANISM Homo sapiens

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 803)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: csapbs-remail.nih.gov  
Tissue Procurement: Dr. Stefan Hanson  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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US-10-047-021-86 (1-303) x CB997292 (1-803)

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Qy 21 LeuileMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40  
Db CTATCATGGAGGAGCATGGCTCAGGACTCCCGGCCCCAGATCTTAGTCCACCCCGAGAC 157  
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
Db CAGCTGTTCAGGGGCCCTGGCCCTGCCAGGATGAGTGGCCGAGCCTCAGGCGACCACT 217  
Qy 61 ProThrIleArgTrpLeuLeuLeuAsnGlyGlnProLeuSerMetValProAspProHis 80  
Db CCACCATTCGCTGTGCTGAATGGGACGCCCTGTAGCATGGTGGCCCGACAGACCCAC 277  
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
Db CACTCTCTGCTGATGGACCCCTCTCTGCTGCTACAGCCCTCTGCGGGGACATGCCAC 337  
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120  
Db GATGGCCAGGCGCTGTCCAGACCTGGGTGTCTACACATGTGAGGCGCAGCAACCGGCTT 397





Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1230)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

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Unpublished

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National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

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Tissue Procurement: Invitrogen

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National Institutes of Health, Mammalian Gene Collection (MGC)

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Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

NIH-MGC <http://mgs.nci.nih.gov/>.

Db 395 GGCACGGCAGTCAGCAGAGCGCTGGCTGTCTGTGGCTGTCTCTCGGGAGGATTTCCAG 454

Qy 141 ILeGlnProArgaspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160

Db 455 ATCCAGCCTCGGACATGGTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 514

Qy 161 ProTyrGlyHisProGluProThrValSerTyrTyrLysAspGlyLysProLeuAlaLeu 180

Db 515 CCCTGGGGCCACCAGAGCCACAGTCTCATGTGGAAAGATGGAAACCCCTGGCCCTC 574

Qy 181 GlnProGlyArgHisThrVal---SerGlyGlySerLeuLeuMetAla--- 195

Db 575 CAGCCGGAAGGCACACAGTGTGCCGGGGGTCCTTGTGGTGGTGGTGGTGGTGGTGGTGG 634

Qy 196 ---ArgAlaGluLys--- 199

Db 635 TTTTCTGGCTAAAGGGCAATTAAACACTGTGTGTCCGCCCGCTTAAACACCCCAAGGCACC 694

Qy 200 ---SerAspGlu---ThrTyr 205

Db 695 CTTGGACAGCCACACACTACAGGGCGCCTTTCTCGGTATGACCCCGCTACATAC 754

Qy 206 MetCysVal---AlaThrAsnSerAlaGlyHisArgGluSerArgAla 220

Db 755 TCATGACCCCTTCCTGCTCCCGGTTCTTCTGGCGCGGTCGCCACCTTACTTTC 814

Qy 221 AlaArgValSerLe---GlnGluProGlnAsp--- 230

Db 815 TCGCGCTCGACAAAGCCACCTCGAGCTTTTACCGCGAGCGCGCAGACTAAGATCCG 874

Qy 231 ---TyrThrGluProValGluLeuAlaValArgGlnGlnGlu 245

Db 875 ACAGACAGTATCTCTACACCGCCCGACGA---TCAGATGGCGCGAGCTCGAA 925

Qy 246 AsnValThrLeuLeuAsnProAspPro--- 254

Db 926 CGGTTCCCTCCGTCACCGTACCGCGGCTCCTCTGTGTATGATCCAGCAGAGAAAT 985

Qy 255 ---AlaGluGlyProLysProArg-ProAlaValTrpLeu---TrpLysVa 270

Db 986 TGGCGCGCATCGGCGGAGGACCCGAA---AGAGCCCGCC---TGCGGAAC 1030

Qy 270 lSerGlyPro\*\*ArgLeuProAsnLeuThrArg 281

Db 1031 CGACGGACATATTAAGCGCCAGATCTATGAAGA 1064

RESULT 13

CB959649

LOCUS

DEFINITION

CB959649

VERSION

CB959649.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 771)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM381 row: 1 column: 13

Alignment Scores:

Pred. No.: 1.92e-67 Length: 1230

Score: 1030.00 Matches: 222

Percent Similarity: 67.05% Conservative: 14

Best Local Similarity: 63.07% Mismatches: 37

Query Match: 64.05% Indels: 79

DB: 12 Gaps: 10

US-10-047-021-86 (1-303) x BM906521 (1-1230)

Qy 1 MetGlySerGlyGlyAspSerLeuGlyArgGlySerLeuProLeuLeuLeu 20

Db 35 ATGGGCTCTGAGAGACAGGCTCTCTGGGGGCGAGGGTTCCTGCTGTCTGCTCTG 94

Qy 21 LeulleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40

Db 95 CTATATCGGAGGATGGCTCAGAGCTCCCGCGCCAGATCTCTAGTCCACCCCGAGAC 154

Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60

Db 155 CAGCTGTGTCCAGGGCCCTGGCCGAGGATGAGCTGCCAAGGCTCAGGCGACCCACCT 214

Qy 61 ProThrIleArgTyrLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80

Db 215 CCCACCATCCCTGGTGTCTGAATGGGCGAGCCCTGAGCATGTGTGCCCGACCCACAC 274

Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100

Db 275 CACCTCTGCTGATGGACCTCTCTGCTACAGCCCTTGTGCGCGGGGACATGCCAC 334

Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120

Db 335 GATGGCAGGCGCTGTTCACAGACTGGGTGTCTACATGTGAGGCGCAGCAACCGGCTT 394

Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140

High quality sequence stop: 628.

## FEATURES

source

1. .771

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30344820"

/tissue\_type="Human Placenta"

/lab\_host="DH10B Tona"

/clone\_lib="NIH MGC 147"

/note="Organ: Placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH MGC library."

BASE COUNT 147 a 246 c 245 g 124 t 9 others

## ORIGIN

## Alignment Scores:

Pred. No.: 2,398-67 Length: 771  
Score: 1025.50 Matches: 197  
Percent Similarity: 89.43% Conservativity: 6  
Best Local Similarity: 86.70% Mismatches: 19  
Query Match: 63.77% Indels: 5  
DB: 14 Gaps: 2

US-10-047-021-86 (1-303) x CB959649 (1-771)

QY 1 MetGlySerGlyGlyValAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeuLeu 20  
DB 66 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGGTTCCTGCTCTGCTCTCTG 125  
QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnLeuValHisProGlnAsp 40  
DB 126 CTCATCTGGGAGGATGGCTCAGACTCCCGCCGCGGAGATCTAGTCCACCCCGAGGAC 185  
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
DB 186 CAGCTGTGTCCAGGGGCTCTGGGCTCCAGGATGAGCTGCCAAGGCTCAGGCCAGCCT 245  
QY 61 ProThrLeuArgTyrLeuLeuAsnGlyGlnProLeuSerMetValProAspProHis 80  
DB 246 CCCACATCCGCTGTGCTGAATGGGAGCCCTTGAGCATGGTCCCGCCAGACCCACAC 305  
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
DB 306 CACCTCTGCTGATGGGACCTTCTGCTGCTACAGCCCTGCGCGGGGACATGCCAC 365  
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120  
DB 366 GATGCCAGGCGCTCTCCACAGACCTGGGTGTCTACATGTGAGGCGCAGCAACCGGCTT 425  
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140  
DB 426 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCTCTCGGGAGGATTTCCAG 485  
QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160  
DB 486 ATCCAGCTCTGGGACATGGTGGCTGTGGGTGAGCAGATTACTCTGGAATGTGGCGG 545  
QY 161 ProTrpGlyHisProGluProThrValSerTrpTyrAspGlyLysProLeuAlaLeu 180  
DB 546 CCTGGGGCCACCCAGAGCCACAGTCTCATGCTGGAAAGATGGAAACCCCTGCGCCCTC 605  
QY 181 GlnProGlyArgHisThr----ValSerGlyGlySerLeuLeuMetAla----- 195  
DB 606 CAGCCCGGAAGGACACACAGTGTCCGGGGGGTCCCTNGCTGTATGGCAANGAGCAGAAGA 665  
QY 196 ArgAlaGluLysSerAspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHis 215

DB 666 AGAGTGGACGAAGGGGACCTTANNCATGTGTGTGGCCANNCCACAGCGCAAGGAAC 725  
QY 216 ArgGluSerArgAlaAlaArg 222  
DB 726 CATAGGGGAGAAAGCCCCCGC 746

## RESULT 14

## CB961529

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1. .798

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="IMAGE:30348011"

## /tissue\_type="pre-eclampsia placenta"

## /lab\_host="DH10B Tona"

## /clone\_lib="NIH MGC 148"

## /note="Organ: placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamH; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH MGC Library."

## BASE COUNT 155 a 261 c 242 g 139 t 1 others

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-10-047-021-86 (1-303) x CB961529 (1-798)

## QY 1 MetGlySerGlyGlyValAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeu 20

## DB 38 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGGTTCCTGCTCTGCTCTGCT 97

## QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnLeuValHisProGlnAsp 40

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Db 98 CTCATCATGGAGGATGGCTCAGAGACTCCCGCCCGCCAGATCTCTAGTCCACCCCGCCAGGAC 157
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 158 CAGTGTTCAGAGCCCTGGCCCTGCCAGATAGCTGCCGAGCTCAGGAGCTCAGGCCACCCACCT 217
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 218 CCCACCATCCGCTGGTGTCTGAATGGGAGCCCTGAGCATGGTGGCCCGCCAGACCCACAC 277
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 278 CACTCTCTGCTGATGGAGCCCTTCTGCTGTACAGCCCTGCTGCGGGGAGCATGCCCCAC 337
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 338 GATGGCCAGGCCCTGTCTCAGACACTGGTGTCTACACATGTGAGGCGAGCACCGGCTT 397
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 398 GGCACGCGAGTCAGACAGAGCGCTCGGCTGTCTGTGCTGTCTCGGAGGATTTCCAG 457
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
Db 458 ATCCAGCCTCGGAGCATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 517
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
Db 518 CCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGAAATCCCTCGGCCCTC 577
Qy 181 GlnProGlyArgHisThrVal---SerGlyGlySerLeuLeuMetAlaArgAlaGluLys 199
Db 578 CCGCCCCGAGGACACAGATGATCCGGGGGGTCTCTGTGTGTGGGCAAGAGCAATAAA 637
Qy 200 SerAsp-----Glu***ThrTyrMetCysValAlaThrAnSerAlaGlyHisArg 216
Db 638 AACAGTTTGACGAAGGAGCCCTTTTGTGTGTGTGGGGCCACCAATCAAGCTCCAGGGGAAA 697
Qy 217 GluSerArgAlaAlaArgValSer 224
Db 698 TTAAGGAGAGAGCCCGCCCAAC 721

RESULT 15
CB961818
LOCUS
DEFINITION AGNCOURT 13665726 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30349135 5', mRNA sequence.
CB961818
VERSION CB961818.1 GI:30217935
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 688)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM392 row: p column: 08
High quality sequence stop: 448.
Location/Qualifiers
1. .688
/organism="Homo sapiens".
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/db_xref="taxon:9606"
/clone="IMAGE:30349135"
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/lab_host="DH10B Tona"
/clone_11b="NIH_MGC_148"
/notes="Organ: placenta; Vector: pBluescriptR; Site 1:
alt-XhoI; Site 2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTCTTTTCTVN-3', size-selected for average insert
size 2.3 kb and normalized to 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
BASE COUNT 126 a 229 c 216 g 116 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 5,36e-64 Length: 688
Score: 980.00 Matches: 191
Percent Similarity: 94.09% Conservative: 0
Best Local Similarity: 94.09% Mismatches: 8
Query Match: 60.95% Indels: 4
DB: 14 Gaps: 2
US-10-047-021-86 (1-303) x CB961818 (1-688)
Qy 1 MetGlySerGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
Db 38 ATGGGCTCTGAGGAGACAGCCCTCTGGGGGGGAGGGTTCCTGCTCTGCTGCTG 97
Qy 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
Db 98 CTATCATGGAGGAGCATGGCTCAGGACTCCCGCCCGCCAGATCTCTAGTCCACCCCGAGAC 157
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 158 CAGCTGTTCAGGGCCCTGGCCCTGCCAGATGAGTGTGGGAGCTCAGGCCCTCAGGCCACCT 217
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 218 CCCACCATCCGCTGGTGTCTGAATGGGAGCCCTGAGCATGGTGGCCCGCCAGACCCACAC 277
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 278 CACTCTCTGCTGATGGAGCCCTTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 337
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
Db 338 GATGGCCAGGCCCTGTCTCAGACACTGGTGTCTACACATGTGAGGCGAGCACCGGCTT 397
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 398 GGCAGGCGAGTCAGACAGAGCGCTCGGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 457
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
Db 458 ATCCAGCCTCGGAGCATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 517
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLys---ProLeuAla 179
Db 518 CCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGAAACCCCTGGGCCCC 577
Qy 180 LeuGlnProGlyArgHisThr---ValSerGlyGlySerLeuLeu---MetAlaArgAla 198
Db 578 TCAGCCCCCGAAAGGACACAGTGTCCGGGGGGGTCCCTGCTGTGTGTGTGTGTGTGTGTGTGT 637
Qy 198 LysLys 199
Db 638 AAAAG 642
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Search completed: January 31, 2004, 15:28:18  
Job time : 1848.41 secs

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**THIS PAGE BLANK (user)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 30, 2004, 15:44:59 ; Search time 35.7513 Seconds  
(without alignments)  
1225.369 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303

Perfect score: 1475

Sequence: 1 QDSPPPQLVHPDQLFQFG.....SGPRLPREALRGQRNTG 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_15Jun03.\*

Result No.	Score	Query Match	Length	DB ID	Description
1	1469	99.6	303	23	ABP62033 Human secreted pro
2	1469	99.6	304	20	AAU12934 Amino acid sequenc
3	1311	88.9	480	22	AAU00501 Human TANGO 330 fo
4	1311	88.9	985	20	AAU41716 Human PRO860 prote
5	1311	88.9	985	21	ABE44272 Human PRO860 (UNQ4
6	1311	88.9	985	24	ABU61102 Human PRO860 polyp
7	1311	88.9	1007	23	ABB97310 Novel human protei
8	1311	88.9	1104	23	AAU99419 Human ECSM4 protei
9	1303	88.3	792	22	AAB95515 Human protein sequ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	1303	88.3	792	22	AAG67430	Amino acid sequenc
11	1029.5	69.8	1015	23	AAU99420	Mouse ECSM4 protei
12	955	64.7	934	22	AAU00500	Human TANGO 330 fo
13	446.5	30.3	753	20	AAW83927	Human T85 protein.
14	446.5	30.3	753	24	ABU04090	Human expressed pr
15	446.5	30.3	1649	20	AAU08404	Human ROBO1 protei
16	446.5	30.3	1649	24	ABU04091	Human expressed pr
17	446.5	30.3	1651	20	AAU13566	Human Robo 1 polyp
18	446.5	30.3	1651	24	ABU04089	Human expressed pr
19	446.5	30.3	1651	24	ABU04092	Human expressed pr
20	446.5	30.3	1651	24	ABU04093	Human expressed pr
21	446.5	30.3	1651	24	ABU04094	Human expressed pr
22	404.5	27.4	1515	23	AAO19185	Human neurotransmi
23	396.5	26.9	1422	23	AAO19179	Human neurotransmi
24	395.5	26.8	1395	20	AAU13563	Drosophila Robo 1
25	395.5	26.8	1395	20	AAU08401	Drosophila sp. ROB
26	395.5	26.8	1395	22	ABW8257	Drosophila melanog
27	354.5	24.0	1297	20	AAU13565	C. elegans Robo po
28	354.5	24.0	1297	20	AAU08403	C. elegans ROBO pr
29	345	23.4	1380	20	AAU08402	Drosophila sp. ROB
30	345	23.4	1381	20	AAU13564	Drosophila Robo 2
31	323	21.9	823	22	ABW61552	Drosophila melanog
32	307	20.8	885	22	ABW61502	Drosophila melanog
33	267.5	18.1	1496	20	AAW81030	Melanoma associate
34	267.5	18.1	1496	21	AAU70469	Human p53 target m
35	267.5	18.1	1496	24	ABU03498	Angiogenesis-assoc
36	267.5	18.1	1498	22	ABW11587	Human peroxidasin
37	265.5	18.0	1463	23	AAO21660	Human secreted pro
38	260.5	17.7	937	22	AAU78714	Human protein SEQ
39	260.5	17.7	952	22	AAU78715	Human protein SEQ
40	260.5	17.7	1267	24	AAE32108	Human cytoskeleton
41	260.5	17.7	1359	24	AAE32109	Human cytoskeleton
42	260.5	17.7	1370	24	ABJ19347	NOVX related prote
43	259	17.6	1527	22	ABW57771	Drosophila melanog
44	250.5	17.0	3931	24	ABU07377	Human protein NOV9
45	240	16.3	1026	23	ABW53276	Human polypeptide

ALIGNMENTS

RESULT 1

ABP62033

ID ABP62033 standard, Protein; 303 AA.

XX AC ABP62033;

XX DT 12-NOV-2002 (first entry)

XX DE Human secreted protein SEQ ID NO 86.

XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;  
KW antiparkinsonian; antiskickling; antianemic; antiarthritic; cancer;  
KW antihemagic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200257420-A2.

XX PD 25-JUL-2002.

XX PF 17-JAN-2002; 2002WO-US01109.

XX PR 18-JAN-2001; 2001US-262066P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Moore PA, Ruben SM, LaFleur DW, Shi Y, Rosen CA, Olsen H;

PI Ebner R, Brewer LA;



```
XX WPI; 2002-599716/64.
DR N-PSDB; ABQ92573.
XX
PT New polynucleotides and polypeptides useful for diagnosing, prognosing,
FT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders
XX
PS Claim 11; Fig 1; 785pp; English.
XX
CC The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
SQ Sequence 303 AA;

Query Match 99.6%; Score 1469; DB 23; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.5e-121;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QDSPPQILVHPDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
Db 28 QDSPPQILVHPDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87

Qy 61 LLLQPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLRDFOIQPRDMV 120
Db 88 LLLQPPARGHAHDGQALSTDLGVYTCEASNRIGTAVSRGARLSVAVLRDFOIQPRDMV 147

Qy 121 AVVGEQFTLCGPPWGHPEPTVSWWKGKPLALQPGHRTVSGSILLMARAEKSDXTYMC 180
Db 148 AVVGEQFTLCGPPWGHPEPTVSWWKGKPLALQPGHRTVSGSILLMARAEKSDXTYMC 207

Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPAVWLX 240
Db 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPAVWLX 267

RESULT 2
AA12934
ID AA12934 standard; Protein; 304 AA.
AC AA12934;
XX
DT 17-JUN-1999 (first entry)
XX
DE Amino acid sequence of a human secreted peptide.
XX
KW Human secreted protein; cancer; immune disorder; infection;
KW inflammatory disorder; skin disorder; tumour; atherosclerosis;
KW restenosis; autoimmune disorder; Alzheimer's disease;
KW peripheral neuropathy; trauma; spinal cord injury; allergy;
KW hematopoietic disorder; skeletal disorder; neurological disorder;
KW arthritic disorder; asthma; immunodeficiency disease; AIDS;
KW transplant rejection; ss.
XX
OS Homo sapiens.
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QY      241 WKVSGPXRPNLTPCSPRLPREARELGRQRTNG 276
      |||||
Db      268 WKVSGPXRPNLTPCSPRLPREARELGRQRTNG 303

RESULT 3
ID      AAU00501
XX      AAU00501 standard; Protein; 480 AA.
AC      AAU00501;
XX      18-JUL-2001 (first entry)
XX      Human TANGO 330 form 2 protein.
XX      Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;
KW      cellular process regulator; gene therapy; astrocyte; cancer;
KW      Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW      cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX      Homo sapiens.
XX
FH      Key
FT      Location/Qualifiers
FT      1..20
FT      /label= Signal_peptide
FT      Modified-site
FT      15..17
FT      /note= "Protein kinase C phosphorylation site"
FT      Domain
FT      21..480
FT      /label= Extracellular_domain
FT      Protein
FT      21..480
FT      /label= Mature_TANGO_330_form_2_protein
FT      Modified-site
FT      30..33
FT      /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
FT      Modified-site
FT      44..47
FT      /note= "Casein kinase II phosphorylation site"
FT      Domain
FT      77..147
FT      /label= Ig-like_domain
FT      Modified-site
FT      93..95
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      100..105
FT      /note= "N-myristylation site"
FT      Modified-site
FT      133..138
FT      /note= "N-myristylation site"
FT      Modified-site
FT      141..146
FT      /note= "N-myristylation site"
FT      Modified-site
FT      148..150
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      152..157
FT      /note= "N-myristylation site"
FT      Modified-site
FT      158..163
FT      /note= "N-myristylation site"
FT      Domain
FT      182..240
FT      /label= Ig-like_domain
FT      Modified-site
FT      230..236
FT      /note= "Tyrosine kinase phosphorylation site"
FT      Modified-site
FT      234..239
FT      /note= "N-myristylation site"
FT      Modified-site
FT      255..258
FT      /note= "Casein kinase II phosphorylation site"
FT      Modified-site
FT      277..280
FT      /note= "Asn is N-glycosylated"
FT      Modified-site
FT      298..300
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      325..330
FT      /note= "N-myristylation site"
FT      Modified-site
FT      343..348
FT      /note= "N-myristylation site"
FT      Modified-site
FT      358..360
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      386..388
FT      /note= "Protein kinase C phosphorylation site"

391..394
/Note= "Asn is N-glycosylated"
408..413
/Note= "N-myristylation site"
420..423
/Note= "Asn is N-glycosylated"
427..430
/Note= "Asn is N-glycosylated"
435..438
/Note= "Casein kinase II phosphorylation site"
456..461
/Note= "N-myristylation site"

WO200123523-A2.
05-APR-2001.
02-OCT-2000; 2000WO-US27202.
30-SEP-1999; 99US-0409634.
(MILL-) MILLENNIUM PHARM INC.
Kirst S, Wrighton N, Fraser CC;
WPI; 2001-235372/24.
N-PSDB; AAS01695.
Isolated secreted proteins and their encoding nucleic acids are used
for diagnosis and treatment of e.g. bacterial and viral infections,
autoimmune diseases and inflammatory disorders -
Claim 9; Fig 14; 261pp; English.
The present sequence representing human TANGO 330 form 2 is
isolated from cDNA clone Jthx181e12 from a human astrocyte cDNA
library. TANGO 330 is 1 of 4 novel human transmembrane proteins.
which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)
and TANGO 480 (AAU00503). The nucleic acids encoding these proteins
are useful as modulating agents in regulating a variety of cellular
processes and can be used to express the proteins in a host cell in
gene therapy applications. Antisense nucleic acid molecules and
expression vectors containing the TANGO nucleic acids are also described.
Diagnostic assays can be used to detect genetic alterations in the TANGO
nucleic acids and to identify compounds that bind to or modulate activity
of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to
monitor protein levels in tissue as a clinical testing procedure.
TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids
and proteins may be used to diagnose, treat and monitor disorders of the
adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They
can also be used to treat cell proliferative disorders (e.g. cancer),
and neurological disorders e.g. Alzheimer's disease.
Sequence 480 AA;
Query Match 88.9%; Score 1311; DB 22; Length 480;
Best Local Similarity 98.8%; Pred No. 2.4e-107;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      1 QDSPPQILVHPQDQLFQGGPGPARMSCRAGOPPTIRWLLNGQPLSMVPPDPHLLPDGT 60
      |||||
Db      59 QDSPPQILVHPQDQLFQGGPGPARMSCRAGOPPTIRWLLNGQPLSMVPPDPHLLPDGT 118
QY      61 LLLLOPPARGHAHDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDQIQPRDV 120
      |||||
Db      119 LLLLOPPARGHAHDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDQIQPRDV 178
QY      121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQGRHTVSGSLMARAEKSDXTYMC 180
      |||||
Db      179 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQGRHTVSGSLMARAEKSDXTYMC 238
QY      181 VATNSAGHRESRAARVSIQEPQDYTEPVVELLAVRIQLENVTLLNPDPAEGKPRPAVWLX 240
      |||||

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Db 239 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGFKPRPAVWLS 298  
QY 241 WKVSGP 246  
Db 299 WKVSGP 304  
RESULT 4  
ID AAY41716 standard; Protein; 985 AA.  
XX AAY41716  
AC AAY41716;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PRO860 protein sequence.  
XX  
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.  
XX  
OS Homo sapiens.  
XX  
PN WO9946281-A2.  
XX  
PD 16-SEP-1999.  
XX  
PF 08-MAR-1999; 99WO-US05028.  
XX  
PR 10-MAR-1998; 98US-0077450.  
PR 11-MAR-1998; 98US-0077632.  
PR 11-MAR-1998; 98US-0077641.  
PR 11-MAR-1998; 98US-0077643.  
PR 12-MAR-1998; 98US-0077791.  
PR 13-MAR-1998; 98US-0078004.  
PR 17-MAR-1998; 98US-0040220.  
PR 20-MAR-1998; 98US-0078886.  
PR 20-MAR-1998; 98US-0078910.  
PR 20-MAR-1998; 98US-0078936.  
PR 20-MAR-1998; 98US-0078933.  
PR 25-MAR-1998; 98US-0079294.  
PR 26-MAR-1998; 98US-0079656.  
PR 27-MAR-1998; 98US-0079663.  
PR 27-MAR-1998; 98US-0079664.  
PR 27-MAR-1998; 98US-0079689.  
PR 27-MAR-1998; 98US-0079728.  
PR 27-MAR-1998; 98US-0079786.  
PR 30-MAR-1998; 98US-0079920.  
PR 30-MAR-1998; 98US-0079923.  
PR 31-MAR-1998; 98US-0080105.  
PR 31-MAR-1998; 98US-0080107.  
PR 31-MAR-1998; 98US-0080165.  
PR 31-MAR-1998; 98US-0080165.  
PR 01-APR-1998; 98US-0080194.  
PR 01-APR-1998; 98US-0080327.  
PR 01-APR-1998; 98US-0080328.  
PR 01-APR-1998; 98US-0080333.  
PR 01-APR-1998; 98US-0080334.  
PR 08-APR-1998; 98US-0081049.  
PR 08-APR-1998; 98US-0081070.  
PR 08-APR-1998; 98US-0081071.  
PR 09-APR-1998; 98US-0081195.  
PR 09-APR-1998; 98US-0081203.  
PR 09-APR-1998; 98US-0081223.  
PR 15-APR-1998; 98US-0081817.  
PR 15-APR-1998; 98US-0081836.  
PR 15-APR-1998; 98US-0081952.  
PR 15-APR-1998; 98US-0081955.  
PR 15-APR-1998; 98US-0082568.  
PR 21-APR-1998; 98US-0082568.  
PR 21-APR-1998; 98US-0082569.  
PR 22-APR-1998; 98US-0082700.  
PR 22-APR-1998; 98US-0082700.  
PR 22-APR-1998; 98US-0082804.  
PR 23-APR-1998; 98US-0082767.  
23-APR-1998; 98US-0082796.  
27-APR-1998; 98US-0083336.  
28-APR-1998; 98US-0083322.  
29-APR-1998; 98US-0083392.  
29-APR-1998; 98US-0083495.  
29-APR-1998; 98US-0083496.  
29-APR-1998; 98US-0083499.  
29-APR-1998; 98US-0083500.  
29-APR-1998; 98US-0083545.  
29-APR-1998; 98US-0083554.  
29-APR-1998; 98US-0083558.  
29-APR-1998; 98US-0083559.  
30-APR-1998; 98US-0083742.  
05-MAY-1998; 98US-0084366.  
06-MAY-1998; 98US-0084414.  
06-MAY-1998; 98US-0084441.  
07-MAY-1998; 98US-0084598.  
07-MAY-1998; 98US-0084600.  
07-MAY-1998; 98US-0084627.  
07-MAY-1998; 98US-0084637.  
07-MAY-1998; 98US-0084639.  
07-MAY-1998; 98US-0084640.  
07-MAY-1998; 98US-0084643.  
13-MAY-1998; 98US-0085323.  
13-MAY-1998; 98US-0085338.  
13-MAY-1998; 98US-0085339.  
15-MAY-1998; 98US-0085573.  
15-MAY-1998; 98US-0085579.  
15-MAY-1998; 98US-0085580.  
15-MAY-1998; 98US-0085582.  
15-MAY-1998; 98US-0085689.  
15-MAY-1998; 98US-0085697.  
15-MAY-1998; 98US-0085700.  
15-MAY-1998; 98US-0085704.  
18-MAY-1998; 98US-0086023.  
22-MAY-1998; 98US-0086392.  
22-MAY-1998; 98US-0086414.  
22-MAY-1998; 98US-0086430.  
22-MAY-1998; 98US-0086486.  
28-MAY-1998; 98US-0087098.  
28-MAY-1998; 98US-0087106.  
28-MAY-1998; 98US-0087208.  
30-JUL-1998; 98US-0094651.  
11-SEP-1998; 98US-0100038.  
(GETH ) GENENTECH INC.  
Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
WPI; 1999-551358/46.  
N-PSDB; AAZ34069.  
XX  
PT New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders -  
XX  
PS Claim 12; Fig 77; 530pp; English.  
XX  
CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as  
CC sources of probes, primers, for chromosome mapping, and for generation  
CC of antisense sequences. They can also be used to create transgenic  
CC animals. The proteins can be used to treat a variety of diseases and  
CC disorders, depending on their function. Diseases that may be treated  
CC include blood coagulation disorders, cancers and cellular adhesion  
CC disorders. They may also be used to raise antibodies. AAZ33891 to  
CC AAZ34338, and AA41685 to AA41774 represent polynucleotide and  
CC polypeptide sequence given in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 985 AA;  
Query Match 88.9%; Score 1311; DB 20; Length 985;



PR	07-OCT-1998;	98WO-US21141.	PR	14-MAY-1999;	99US-0380137.	XX	(GETH ) GENENTECH INC.	PA	30-JUL-2001;	2001US-0918585.	XX	
PR	20-NOV-1998;	98WO-US24855.	PR	25-AUG-1999;	99US-0380138.	XX		PI	Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;	PI		
PR	05-JAN-1999;	99WO-US00106.	PR	25-AUG-1999;	99US-0380142.	XX		PI	Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies -	PI		
PR	08-MAR-1999;	99WO-US05028.	PR	27-NOV-2000;	2000US-0792338.	XX		PI	Claim 12; Fig 77; 459pp; English.	PI		
PR	10-MAR-1999;	99WO-US05190.	PR	20-DEC-2000;	2000US-0723749.	XX		XX	The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The bioactive molecule maybe a toxin, radiolabel or antibody, and causes apoptosis or death of the cell. The PRO polypeptides are useful for treating immune disorders, diabetes or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system disorders, kidney disorders, bone and cartilage disorders or arthritis, tumours, and wound healing. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy.	XX		
PR	14-MAY-1999;	99WO-US10733.	PR	20-DEC-2000;	2000US-0747259.	XX		XX	ABU61071-ABU61164 represent the human PRO polypeptides of the invention.	XX		
PR	02-JUN-1999;	99WO-US12252.	PR	22-MAR-2001;	2001US-0816744.	XX		XX	Note: The sequence data for this patent, was obtained in electronic format directly from the USPTO web site at <a href="http://seqdata.uspto.gov/psipSIDEntry.html">seqdata.uspto.gov/psipSIDEntry.html</a> .	XX		
PR	30-NOV-1999;	99WO-US28313.	PR	22-MAR-2001;	2001US-0816920.	XX		XX	Query Match 88.9%; Score 1311; DB 24; Length 985; Best Local Similarity 98.8%; Pred. No. 5.7e-107; Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	XX		
PR	02-DEC-1999;	99WO-US28551.	PR	10-MAY-2001;	2001US-0854208.	XX		XX	QY 1 QDSPPQILVHPDQDLFOGPGPARMSCRAGOPPTIRWLNGQPLSVVPPDPHLLPDGT 60	QY		
PR	16-DEC-1999;	99WO-US30095.	PR	01-JUN-2001;	2001US-0872035.	XX		XX	DB 6 QDSPPQILVHPDQDLFOGPGPARMSCRAGOPPTIRWLNGQPLSVVPPDPHLLPDGT 65	DB		
PR	30-DEC-1999;	99WO-US31274.	PR	05-JUN-2001;	2001US-0874503.	XX		XX	QY 61 LLLLOPPARGHAHDQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLRDFQIQPRDMV 120	QY		
PR	05-JAN-2000;	2000WO-US00219.	PR	14-JUN-2001;	2001US-0882636.	XX		XX	DB 66 LLLLOPPARGHAHDQALSTDLGVYTCEASNRGLTAVSRGARLSVAVLRDFQIQPRDMV 125	DB		
PR	06-JAN-2000;	2000WO-US00376.	PR	19-JUN-2001;	2001US-0886342.	XX		XX	QY 121 AVVGEQFTLECGPPMGHPHPTVSWWKGKPLALQFGHRTVSGGSLLMARAEKSDXTYMC 180	QY		
PR	11-FEB-2000;	2000WO-US03565.	PR	30-JUL-2001;	2001US-0918585.	XX		XX	DB 126 AVVGEQFTLECGPPMGHPHPTVSWWKGKPLALQFGHRTVSGGSLLMARAEKSDXTYMC 185	DB		
PR	18-FEB-2000;	2000WO-US04341.	PR			XX		XX				
PR	24-FEB-2000;	2000WO-US05004.	PR			XX		XX				
PR	02-MAR-2000;	2000WO-US05841.	PR			XX		XX				
PR	10-MAR-2000;	2000WO-US06319.	PR			XX		XX				
PR	21-MAR-2000;	2000WO-US07532.	PR			XX		XX				
PR	30-MAR-2000;	2000WO-US08439.	PR			XX		XX				
PR	17-MAY-2000;	2000WO-US13705.	PR			XX		XX				
PR	22-MAY-2000;	2000WO-US14042.	PR			XX		XX				
PR	30-MAY-2000;	2000WO-US14941.	PR			XX		XX				
PR	02-JUN-2000;	2000WO-US15264.	PR			XX		XX				
PR	28-JUL-2000;	2000WO-US20710.	PR			XX		XX				
PR	24-AUG-2000;	2000WO-US23328.	PR			XX		XX				
PR	01-DEC-2000;	2000WO-US32678.	PR			XX		XX				
PR	20-DEC-2000;	2000WO-US34956.	PR			XX		XX				
PR	28-FEB-2001;	2001WO-US06520.	PR			XX		XX				
PR	22-MAR-2001;	2001WO-US09552.	PR			XX		XX				
PR	25-MAY-2001;	2001WO-US17092.	PR			XX		XX				
PR	01-JUN-2001;	2001WO-US17800.	PR			XX		XX				
PR	20-JUN-2001;	2001WO-US19692.	PR			XX		XX				
PR	29-JUN-2001;	2001WO-US21066.	PR			XX		XX				
PR	09-JUL-2001;	2001WO-US21735.	PR									



Query Match 88.9%; Score 1311; DB 23; Length 1104;  
Best Local Similarity 98.8%; Pred. No. 6.5e-107;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDSPPQILVHPDQQLFOGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
Db 28 QDSPPQILVHPDQQLFOGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87

Qy 61 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRGLTAVSRGRLSVAVLRDFOQPRDMV 120  
Db 88 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRGLTAVSRGRLSVAVLRDFOQPRDMV 147

Qy 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRTVSGSLLMARAESDXTYMC 180  
Db 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRTVSGSLLMARAESDXTYMC 207

Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLNPDPAEGPKPPAVWLX 240  
Db 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLNPDPAEGPKPPAVWLX 267

Qy 241 WKVSGP 246  
Db 268 WKVSGP 273

## RESULT 9

AAB95515  
ID AAB95515 standard; Protein; 792 AA.

XX AC AAB95515;

XX DT 26-JUN-2001 (first entry)

XX DE Human protein sequence SEQ ID NO:18085.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX OS Homo sapiens.

XX XX EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

XX Claim 8; SEQ ID 18085; 2537pp + CD ROM; English.

XX PS The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence and the oligonucleotide is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAB95515 to AAB95515 and AAB95515 to AAB95515 represent human cDNA sequences; AAB95515 to AAB95515 represent human amino acid sequences; and AAB95515 to AAB95515 represent oligonucleotides, all of which are used in the exemplification of the present invention.

SQ Sequence 792 AA;

Query Match 88.3%; Score 1303; DB 22; Length 792;  
Best Local Similarity 98.4%; Pred. No. 2.2e-106;  
Matches 242; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QDSPPQILVHPDQQLFOGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
Db 28 QDSPPQILVHPDQQLFOGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87

Qy 61 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRGLTAVSRGRLSVAVLRDFOQPRDMV 120  
Db 88 LLLLOPPARGHAHDGQALSTDLGVYTCEASNRGLTAVSRGRLSVAVLRDFOQPRDMV 147

Qy 121 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRTVSGSLLMARAESDXTYMC 180  
Db 148 AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRTVSGSLLMARAESDXTYMC 207

Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLNPDPAEGPKPPAVWLX 240  
Db 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAIVRIQLENVTLNPDPAEGPKPPAVWLX 267

Qy 241 WKVSGP 246  
Db 268 WKVSGP 273

## RESULT 10

AAG67430  
ID AAG67430 standard; Protein; 792 AA.

XX AC AAG67430;

XX DT 26-NOV-2001 (first entry)

XX DE Amino acid sequence of a human protein kinase/protein phosphatase.

XX KW Human; protein kinase; protein phosphatase; signal transduction;  
XX KW intracellular signalling pathway.

XX OS Homo sapiens.

XX PN WO200109345-A1.

XX PD 08-FEB-2001.

XX PF 28-JUL-2000; 2000WO-JP05060.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 18-OCT-1999; 99US-0159590.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 17-FEB-2000; 2000US-0183322.

XX PR 02-MAY-2000; 2000JP-0183767.

XX (HELI-) HELIX RES INST.

XX PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;



PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;  
PI Senoo C, Nezu J;  
XX  
XX  
XX WPI: 2001-564736/63.  
DR N-PSDB; AAH78073.  
XX

PT New genes encoding protein kinase and protein phosphatase, useful\* for  
PT identifying modulators which can be used to treat human or animal  
PT disorders associated with the expression or function of these enzymes -  
XX.  
PS Claim 2; Page 175-180; 336pp; Japanese.

XX The present sequence represents a human protein kinase/protein  
CC phosphatase. The polypeptides are expected to participate in signal  
CC transduction in cells. The kinase phosphatases are connected with  
CC intracellular signalling pathways. Antisense oligonucleotides and  
CC compounds identified by screening (agonists or antagonists) can be  
CC used to treat human or animal disorders associated with the expression  
CC or function of the protein. In addition, the polypeptides may be used  
CC as target molecules for drug development.

XX Sequence 792 AA;

Query Match 88.3%; Score 1303; DB 22; Length 792;  
Best Local Similarity 98.4%; Pred. No. 2.2e-106;  
Matches 242; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFQGGPARMSCRAGSQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
DB 28 QDSPPQILVHPQDQLFQGGPARMSCRAGSQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 87  
QY 61 LLLLOPPARGHADGQALSTDLGVYTCEASNRGTAVSRGARLSVAVLRDFQIQPRDMV 120  
DB 88 LLLLOPPARGHADGQALSTDLGVYTCEASNRGTAVSRGARLSVAVLRDFQIQPRDMV 147  
QY 121 AVVGEQFTLECGPPMGHPPTVSWWKGKPLALQPGRTVSGSLLMARAESDXTYMC 180  
DB 148 AVVGEQFTLECGPPMGHPPTVSWWKGKPLALQPGRTVSGSLLMARAESDXTYMC 207  
QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240  
DB 208 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 267  
QY 241 WKVSGP 246  
DB 268 WKVSGP 273

RESULT 11  
AAU99420  
ID AAU99420 standard; Protein; 1015 AA.

XX AAU99420;

XX 07-OCT-2002 (first entry)

XX Mouse ECSM4 protein #1.

XX Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature;  
KW imaging vascular endothelium; proliferative disease; cancer;  
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;  
KW endothelial damage; tumour neovasculature; cardiac disease;  
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;  
KW cardiant.

XX Mus sp.

XX WO200236771-A2.

XX 10-MAY-2002.

XX 06-NOV-2001; 2001WO-GB04906.

PR 06-NOV-2000; 2000US-245566P.  
PR 07-MAR-2001; 2001US-273662P.  
XX  
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Bicknell R, Huminiacki L;

XX WPI: 2002-508120/54.

XX N-PSDB; ABK87138.

PT Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for  
PT imaging, diagnosing and treating a condition involving vascular  
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -  
XX  
XX Disclosure; Fig 13; 248pp; English.

XX The present invention relates to endothelial cell-specific molecule 4  
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4  
CC proteins are useful for imaging vascular endothelium in the body of  
CC an individual, and for diagnosing and treating a proliferative  
CC disease or condition involving the vascular endothelium (preferably,  
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,  
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in  
CC the manufacture of diagnostic or prognostic agent for such conditions.  
CC The proteins are also useful for detecting endothelial damage or  
CC activation, detecting a tumour or tumour neovasculature, cardiac  
CC disease, or endometriosis by detecting the amount of ECSM4 present in  
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in  
CC gene therapy for treating a hypoxic condition such as cancer, cardiac  
CC disease, endometriosis or atherosclerosis and in the manufacture of  
CC medicaments for treating the above disease. The sequences are useful  
CC for modulating angiogenesis in an individual. The present sequence  
CC represents a mouse ECSM4 protein.

XX Sequence 1015 AA;

Query Match 69.8%; Score 1029.5; DB 23; Length 1015;  
Best Local Similarity 78.5%; Pred. No. 4.3e-82;  
Matches 193; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

QY 2 DSSPQILVHPQDQLFQGGPARMSCRAGSQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 61

DB 39 DSSPQILVHPQDQLFQGGPARMSCRAGSQPPPTIRWLLNGQPLSMATPDLHYLLPDGT 98

QY 62 LLLLOPPARGHADGQ-ALSTDLGVYTCEASNRGTAVSRGARLSVAVLRDFQIQPRDMV 120

DB 99 LLHRPSVQGRPDQDNILSAILGVYVTCASNRGTAVSRGARLSVAVLRDFQIQPRDTV 158

QY 121 AVVGEQFTLECGPPMGHPPTVSWWKGKPLALQPGRTVSGSLLMARAESDXTYMC 180

DB 159 AVVGEQFTLECGPPMGHPPTVSWWKGKPLALQPGRTVSGSLLMARAESDXTYMC 218

QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240

DB 219 MATNNAQRESRAARVSIQESQDHKEHLELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 278

QY 241 WKVSGP 246

DB 279 WKVSGP 284

RESULT 12

AAU00500

ID AAU00500 standard; Protein; 934 AA.

XX AAU00500;

XX 18-JUL-2001 (first entry)

XX Human TANGO 330 form 1 protein.

XX Human; TANGO 315; clone jthaa060g22; TANGO 330; TANGO 437; TANGO 480;  
KW cellular process regulator; gene therapy; adrenal gland; cancer;



Claim 9; Fig 13; 261pp; English.

The present sequence representing human TANGO 330 form 1 is isolated from cDNA clone jthaa060g22 from a human adrenal gland CDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502) and TANGO 480 (AAU00503). The nucleic acids encoding these proteins are useful as modulating agents in regulating a variety of cellular processes and can be used to express the proteins in a host cell in gene therapy applications. Antisense nucleic acid molecules and expression vectors containing the TANGO nucleic acids are also described. Diagnostic assays can be used to detect genetic alterations in the TANGO nucleic acids and to identify compounds that bind to or modulate activity of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to monitor protein levels in tissue as a clinical testing procedure. TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids and proteins may be used to diagnose, treat and monitor disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They can also be used to treat cell proliferative disorders (e.g. cancer), and neurological disorders e.g. Alzheimer's disease.

Sequence 934 AA;

Query Match 64.7%; Score 955; DB 22; Length 934;

Best Local Similarity 98.9%; Pred. No. 1.5e-75;

Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 66 PPARGHAGDQALSTDLGVYTCESNRLGTAVSRGARSVAVLREDFQIQPRDMVAVGGE 125

Db 20 PPARGHAGDQALSTDLGVYTCESNRLGTAVSRGARSVAVLREDFQIQPRDMVAVGGE 79

QY 126 QFTLECGPWGHPPTVSWWKGKPLALQPGRTVSGSLLMARAEKSDXTYMCVATNS 185

Db 80 QFTLECGPWGHPPTVSWWKGKPLALQPGRTVSGSLLMARAEKSDXTYMCVATNS 139

QY 186 AGHRSRAARVSIQSPQDYTEPVELLAVRIQLENTVLNPDPAEGKPPPAVLWKVSG 245

Db 140 AGHRSRAARVSIQSPQDYTEPVELLAVRIQLENTVLNPDPAEGKPPPAVLWKVSG 199

QY 246 P 246

Db 200 P 200

RESULT 13

AAW83927

ID AAW83927 standard; Protein; 753 AA.

XX AC AAW83927;

XX DT 01-MAR-1999 (first entry)

XX DE Human T85 protein.

XX KW T85; FHMB-SD4; FMHV-SD4; human; neurological disorder; therapy;

XX KW diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT Protein /label= Sig\_peptide

FT Protein /label= Mat\_protein

FT Region 525..610

FT /note= "has homology to a fibronectin type III domain"

FT Region 638..727

FT /note= "has homology to a fibronectin type III domain"

FT Region 43..101

FT /note= "has homology to a Ig superfamily domain"

FT Region 145..203

FT Region /note= "has homology to a Ig superfamily domain" 237..298

FT Region /note= "has homology to a Ig superfamily domain" 329..394

FT Region /note= "has homology to a Ig superfamily domain" 433..491

FT Peptide /note= "has homology to a Ig superfamily domain" 247..249

FT Domain /note= "RGD motif" 516..600

FT /note= "cytokine receptor homology N-terminal domain"

WO9848051-A2.

29-OCT-1998.

17-APR-1998; 98WO-US07714.

10-OCT-1997; 97US-0062017.

18-APR-1997; 97US-0044746.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Holtzman D, McCarthy SA;

WPI; 1999-024021/02.

N-PSDB; AAV69278.

New isolated human FTHMA-070 and T85 proteins - used to develop

products for the diagnosis and therapy of disorders involving

cellular processes, e.g. neuronal development.

Claim 31; Fig 3; 127pp; English.

This is the amino acid sequence of a novel human protein designated

T85, and also referred to as FMHB-6D4 and FMHB-SD4. T85 CDNA (see

AAV69278) was identified in a human foetal brain cDNA library using a

screen designed to identify genes encoding proteins having a

functional signal sequence. T85 nucleic acids and polypeptides of

the invention are useful as modulating agents in regulating a

variety of cellular processes. They can be used for identifying

compounds which bind to or modulate the activity of the polypeptides

(claimed). They can also be used in screening assays, detection

assays (e.g. chromosomal mapping, tissue typing, forensic biology),

predictive medicine (e.g. diagnostic assays, prognostic assays,

monitoring clinical trials, and pharmacogenomics), and methods of

treatment (e.g. therapeutic and prophylactic) e.g. for neurological

disorders.

XX SQ Sequence 753 AA;

Query Match 30.3%; Score 446.5; DB 20; Length 753;

Best Local Similarity 41.7%; Pred. No. 9.2e-31;

Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

QY 1 QDSPQILVHPQDLFCQGGPARMSCRASGPPPTIRLLNGQLSPMVPDPHH---LLP 57

Db 25 EDPFPRIVEHPSDLIVSKGEPTALNCKAEGRTPTIETKGGERVETDKDPRSRMLLP 84

QY 58 DDTLLLLQPPARGHAHQALSTDLGVYTCESNRLGTAVSRGARSVAVLREDFQIQPR 117

Db 85 SGLFFLR-----IVHGKSRPDEGVVVCARNVYGEAVSHNASLEVALRDDFRQNS 138

QY 118 DMVAVVGQFTLECGPPWGHPEPTVSWWKGKPLALQPGRTVSGSLLMARAEKSDXT 177

Db 139 DMVAVGEPVAVMECPPRGHPPTISWKGKSDPLDKDERTIRGKMLITITRKSADGK 198

QY 178 YMCVATNSAGHRESRAARVSIQSPQDYTEPVELLAVRI 215

Db 199 YVCVGTNMVGERESEVAELTVLERPSFVKRPSNLAVTV 236

```
RESULT 14
ABU04090
ID ABU04090 standard; Protein; 753 AA.
XX
AC ABU04090;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #756.
XX
KW Translational profiling; expressed protein tag; EPT; kinase;
KW phosphatase; protease; receptor; transcription factor; cancer; MHC;
KW cytoskeletal proteins; receptors or transcription factors); useful for
KW major histocompatibility complex; myeloma; colon cancer;
KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US09671.
XX
PR 28-MAR-2001; 2001US-279495P.
XX
PR 21-MAY-2001; 2001US-292544P.
XX
PR 08-AUG-2001; 2001US-310801P.
XX
PR 01-OCT-2001; 2001US-326370P.
XX
PR 04-DEC-2001; 2001US-336780P.
XX
PR 20-FEB-2002; 2002US-358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
PT or leukemia -
XX
PS Example 2; SEQ ID No 756; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor.
CC The polypeptide is useful as an immunogenic composition for eliciting
CC in a mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to
CC this polypeptide, is useful for treating cancer. The polypeptide is
CC also useful for identifying compounds that binds to a naturally
CC processed class I or class II MHC-binding polypeptide. The polypeptides
CC and polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling.
CC Note: This sequence does not appear in the printed specification but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 753 AA;
Query Match 30.3%; Score 446.5; DB 24; Length 753;
Best Local Similarity 41.7%; Pred. No. 9.2e-31;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;
Qy 1 QDSPPQILVHPDQDLFOGPGPARMSCRAGQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 25 EDFPPRIVEHPSDLIIVSKGEPATLNCKAEGRPTTIWYKGERVETDKDPRSHRMLLP 84

RESULT 15
AAY08404
ID AAY08404 standard; Protein; 1649 AA.
XX
AC AAY08404;
XX
DT 24-JUL-1999 (first entry)
XX
DE Human ROBO1 protein.
XX
KW ROBO1; ROBO2; roundabout; nerve guidance; human; murine; cell function;
KW cell morphology; screening assay.
XX
OS Homo sapiens.
XX
PN WO9920764-A1.
XX
PF 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22164.
XX
PR 14-NOV-1997; 97US-0971172.
XX
PR 20-OCT-1997; 97US-0062921.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Goodman CS, Kidd T, Mitchell KJ, Tear G;
XX
DR WPI; 1999-312615/26.
XX
DR N-PSDB; AAX08404.
XX
PT Robo polypeptides, a new immunoglobulin superfamily member
XX
PS Claim 1; Page 65-71; 80pp; English.
XX
CC This invention describes novel Robo (roundabout) polypeptides, involved
CC in nerve guidance which have been isolated from Drosophila sp.,
CC C. elegans, human and murine samples. The products of the invention can
CC be used to raise anti-Robo antibodies, which can be used to modulate cell
CC function or morphology. The Robo polynucleotides and fragments are useful
CC as probes and primers and for production of the Robo polypeptides. The
CC probes and primers are also useful in screening assays.
XX
SQ Sequence 1649 AA;
Query Match 30.3%; Score 446.5; DB 20; Length 1649;
Best Local Similarity 41.7%; Pred. No. 2.4e-30;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;
Qy 1 QDSPPQILVHPDQDLFOGPGPARMSCRAGQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPPRIVEHPSDLIIVSKGEPATLNCKAEGRPTTIWYKGERVETDKDPRSHRMLLP 123

58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLCTAVSRGARLSVAVLRDFQIQPR 117
Db 85 SGSLLFFLR-----IVHGRKSRPDEGVYVCVARNYLGEAVSHNASLEVAIILRDDFRQNPS 138

118 DMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAEKSDEXT 177
Db 139 DMVAVGEPAVMECQPPRGHPPTISWKDGSPLDDKDERITIRGGKLMITYTRKSDAGK 198

178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215
Db 199 YVCVGTNMVGERSEVAELTVLRPSFVKRPSNLAVTV 236

RESULT 15
AAY08404
ID AAY08404 standard; Protein; 1649 AA.
XX
AC AAY08404;
XX
DT 24-JUL-1999 (first entry)
XX
DE Human ROBO1 protein.
XX
KW ROBO1; ROBO2; roundabout; nerve guidance; human; murine; cell function;
KW cell morphology; screening assay.
XX
OS Homo sapiens.
XX
PN WO9920764-A1.
XX
PF 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22164.
XX
PR 14-NOV-1997; 97US-0971172.
XX
PR 20-OCT-1997; 97US-0062921.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Goodman CS, Kidd T, Mitchell KJ, Tear G;
XX
DR WPI; 1999-312615/26.
XX
DR N-PSDB; AAX08404.
XX
PT Robo polypeptides, a new immunoglobulin superfamily member
XX
PS Claim 1; Page 65-71; 80pp; English.
XX
CC This invention describes novel Robo (roundabout) polypeptides, involved
CC in nerve guidance which have been isolated from Drosophila sp.,
CC C. elegans, human and murine samples. The products of the invention can
CC be used to raise anti-Robo antibodies, which can be used to modulate cell
CC function or morphology. The Robo polynucleotides and fragments are useful
CC as probes and primers and for production of the Robo polypeptides. The
CC probes and primers are also useful in screening assays.
XX
SQ Sequence 1649 AA;
Query Match 30.3%; Score 446.5; DB 20; Length 1649;
Best Local Similarity 41.7%; Pred. No. 2.4e-30;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;
Qy 1 QDSPPQILVHPDQDLFOGPGPARMSCRAGQPPPTIRWLLNGQPLSMVPPDPHH---LLP 57
Db 64 EDFPPRIVEHPSDLIIVSKGEPATLNCKAEGRPTTIWYKGERVETDKDPRSHRMLLP 123

58 DGTLLLLQPPARGHAHDGQALSTDLGVYTCASNRLCTAVSRGARLSVAVLRDFQIQPR 117
Db 124 SGSLLFFLR-----IVHGRKSRPDEGVYVCVARNYLGEAVSHNASLEVAIILRDDFRQNPS 177

118 DMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAEKSDEXT 177
Db 118 DMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAEKSDEXT 177
```

Db 178 DVMVAVGEPAVMECOPPRGHPEPTISWKXKGSPLDDKDERITIRGGKLMITYTRKSDAGK 237  
Qy 178 YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI 215  
Db 238 YVCVGTNNVGERESEVAELTVLERPSFVKRPSNLATV 275

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OM protein - protein search, using sw model

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(without alignments)  
844.758 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/prodata/1/1aa/5B-COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/6A-COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/6B-COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCTUS-COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446.5	30.3	1651	US-09-540-245A-18	Sequence 18, Appl
2	395.5	26.8	1395	US-09-540-245A-15	Sequence 15, Appl
3	354.5	24.0	1297	US-09-540-245A-17	Sequence 17, Appl
4	345	23.4	1381	US-09-540-245A-16	Sequence 16, Appl
5	251	17.0	630	US-08-752-307B-14	Sequence 14, Appl
6	251	17.0	630	US-09-707-802-14	Sequence 14, Appl
7	251	17.0	630	US-09-991-326-14	Sequence 14, Appl
8	228	15.5	607	US-08-752-307B-12	Sequence 12, Appl
9	228	15.5	607	US-09-707-802-12	Sequence 12, Appl
10	228	15.5	607	US-09-991-326-12	Sequence 12, Appl
11	219	14.8	596	US-08-752-307B-13	Sequence 13, Appl
12	219	14.8	596	US-09-707-802-13	Sequence 13, Appl
13	219	14.8	596	US-09-991-326-13	Sequence 13, Appl
14	218.5	14.8	1501	US-08-447-464-3	Sequence 3, Appl
15	218.5	14.8	1501	US-08-716-679-3	Sequence 3, Appl
16	206.5	14.0	1911	US-08-348-006B-5	Sequence 5, Appl
17	206.5	14.0	1911	US-08-800-825A-5	Sequence 5, Appl
18	206.5	14.0	1911	US-09-158-657-5	Sequence 5, Appl
19	206.5	14.0	1911	PCT-US94-10166-5	Sequence 5, Appl
20	206	14.0	1447	US-09-041-886-25	Sequence 25, Appl
21	206	14.0	1447	PCT-US94-05277-2	Sequence 2, Appl
22	198.5	13.5	615	US-08-752-307B-9	Sequence 9, Appl
23	198.5	13.5	615	US-09-707-802-9	Sequence 9, Appl
24	198.5	13.5	615	US-09-991-326-9	Sequence 9, Appl
25	194.5	13.2	612	US-08-752-307B-11	Sequence 11, Appl
26	194.5	13.2	612	US-09-707-802-11	Sequence 11, Appl
27	194.5	13.2	612	US-09-991-326-11	Sequence 11, Appl

28	194.5	13.2	1268	4	US-08-506-296B-28	Sequence 28, Appl
29	192	13.0	1091	3	US-08-986-485-5	Sequence 5, Appl
30	191	12.9	1260	4	US-08-506-296B-21	Sequence 21, Appl
31	189	12.8	946	5	PCT-US95-08493-13	Sequence 13, Appl
32	188.5	12.8	1101	3	US-08-986-485-2	Sequence 2, Appl
33	186	12.6	416	4	US-09-638-649-1	Sequence 1, Appl
34	185	12.5	611	2	US-08-752-307B-10	Sequence 10, Appl
35	185	12.5	611	4	US-09-707-802-10	Sequence 10, Appl
36	185	12.5	611	4	US-09-991-326-10	Sequence 10, Appl
37	185	12.5	1253	4	US-08-506-296B-14	Sequence 14, Appl
38	175.5	11.9	1209	4	US-09-130-158A-2	Sequence 2, Appl
39	175	11.9	462	2	US-08-752-307B-7	Sequence 7, Appl
40	175	11.9	462	4	US-09-707-802-7	Sequence 7, Appl
41	175	11.9	462	4	US-09-991-326-7	Sequence 7, Appl
42	175	11.9	465	2	US-08-752-307B-5	Sequence 5, Appl
43	175	11.9	465	4	US-09-707-802-5	Sequence 5, Appl
44	175	11.9	465	4	US-09-991-326-5	Sequence 5, Appl
45	175	11.9	1266	4	US-08-506-296B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-540-245A-18  
; Sequence 18, Application US/09540245A  
; Patent No. 6270984  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey  
; APPLICANT: Kid, Thomas  
; APPLICANT: Brose, Katja  
; APPLICANT: Tessier-Lavigne, Marc  
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions  
; FILE REFERENCE: B98-031-3  
; CURRENT APPLICATION NUMBER: US/09/540,245A  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 60/065,544  
; PRIOR FILING DATE: 1997-11-14  
; PRIOR APPLICATION NUMBER: 60/081,057  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1651  
; TYPE: PRT  
; ORGANISM: human  
US-09-540-245A-18

Query Match	30.3%	Score	446.5	DB 3	Length	1651			
Best Local Similarity	41.7%	Pred. No.	7.7e-36						
Matches	91	Conservative	31	Mismatches	87	Indels	9	Gaps	2
QY	1	QDSPPOILVHPDQLFQGP	PARMSCRASQPPPTIRWLLNGCPLSMVPPDPHH---	LLP	57				
Db	64	EDFPRIIVEHPSDLIVSGEPATLNCKAEGRTPTIEWYKGGVETDKDDPRSHRMLLP	123						
QY	58	DTLLLLLOPPARGHAHDQALSTDLGVYTCASNRLGTAVSRGARLSVAVLRDEFQIQPR	117						
Db	124	SGSLFFLR-----IVHGKSRPDEGVYCVARNYLGEAVSNASLEVAILRRDQFRQPS	177						
QY	118	DMVAVVGQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHTVSGSLLMARAESKDEXT	177						
Db	178	DMVAVGPAVMCEQPPRGHPERTISWKKDGSPLDDKDERITIRGKKLMITYTRKSDAGK	237						
QY	178	YMCVATNSAGHRESAARVSIQEPDYTEPEVLLAVRI	215						
Db	238	YVCVTNNVGERSESEVABLTVLERPSFVKRPSNLAVTV	275						

RESULT 2

US-09-540-245A-15  
; Sequence 15, Application US/09540245A  
; Patent No. 6270984



```

; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-15

Query Match 26.8%; Score 395.5; DB 3; Length 1395;
Best Local Similarity 37.1%; Pred. No. 8.1e-31;
Matches 92; Conservative 35; Mismatches 100; Indels 21; Gaps 6;

Qy 1 QDSPPQILVHPDQQLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLL-LPDG 59
Db 52 QYQSPRIIEHPIDVVSRSRGPATLNC---GAKPSTAKITWYKDGQPVITNKQVNSHRIVLDTG 86

Qy 60 TLLILQPPARGHAHDGQALSTDLGVYTCESNRNLGTAVSRGARLSVAVLRDFOIQPRDM 119
Db 112 ALFFVTRTQWQKEQDG-----GEYWCVKNRVQAVSRHASLQIALVLRDDFRVEPKDT 164

Qy 120 VAVVGEQFTLSCGPPWGHPEPTVSWKDGKPL-----ALQGRHT-----VSGSLLMARAE 171
Db 165 RVAKGETALLCGPPKGPPEPTLWIKDGVPLDLDKAMSGASSRVRIVDGNLLISNVE 224

Qy 172 KSDEXTYMCVATNSAGHRESRAARVSIQ-EPQDYTEPVELLAVRIQLENVTLNPDPAEG 230
Db 225 PIDEGNYKICIAQNLVGTRESSYAKLIVQVKPYFMKEPKD-----QVMLYGGQTATFHCVGG 280

Qy 231 PKRPAVW 238
Db 281 DPPKVLW 288

RESULT 3
US-09-540-245A-17
; Sequence 17, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-245A-17

Query Match 24.0%; Score 354.5; DB 3; Length 1297;
Best Local Similarity 34.0%; Pred. No. 9.7e-27;
Matches 91; Conservative 31; Mismatches 102; Indels 46; Gaps 8;

Qy 5 PQILVHPDQQLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 64
Db 4 PRIIEHPMDITVPKNDPFTFCNQAEQNPTFTIQWFKDGRKLTDTGSHRIMLPAGGLPFL 63

Qy 65 QPPARGHAHDGQALSTDLGVYTCESNRNLGTAVSRGARLSVAVLRDFOIQPRDMVAVG 124
Db 64 KV-----IHSRR--ESDAGTYWCEAKNEFGVARSNATLQVAVLRDEFERLEPANTRVAQ 116

Qy 125 EQFTLECGPPWGHPEPTVSWKDGKPLALQGR--HTVSGSLLMARAEKSDEXTYMCVA 182
Db 117 EVALMECCAPRGSPPEQISWRKNGQTLNLVGNKRIRIVDGNLAIQARQSDDDGRYQCVV 176

Qy 183 TNSAGHRESRAARVS-----IQEPQDYTEPVELLAV-----RIQLENVTLNPDPAEGPK 232
Db 177 KVVVGTRESATAFLKVVHRPFLIRGPQNTAVGVSSVVFQCR-----GGD 222

Qy 233 PRPAVWLXWKGVPXRLPNLTRPCSGPRLP 262
Db 223 PLPDV--LWR-----RTASGGNMP 239
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Matches 96; Conservative 44; Mismatches 101; Indels 41; Gaps 11;

Qy 5 PQILVHPDQQLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDG-G 59
Db 30 PVIEHPIDVVSRSRGPATLNC---GAKPSTAKITWYKDGQPVITNKQVNSHRIVLDTG 86

Qy 60 TLLILQPPARGHAHDGQALSTDLGVYTCESNRNLGTAVSRGARLSVAVLRDFOIQPRDM 119
Db 87 SLFLKYNVSGKNGKD-----SDAGAYYCVASNEHEGKSVKSLKLAHLREDFRVRPTV 141

Qy 120 VAVVGEQFTLSCGPPWGHPEPTVSWKDGKPLALQGRHTV-SGGSLLMARAEKSDEXT 177
Db 142 QALGGENAVLECSPPRGFPFVVSRRKDKELRIQDMPRVTLHSDGNLIIDPVDSDSGT 201

Qy 178 YMCVATNSAGHRESRAARVSI-----QEPQDYTEPVELLAVRIQLENVTLNPDPAEG 230
Db 202 YQCVANNMVGERSVNSPARLSVFEKPKFEQBPQKMT-----VDVGAALVDFCRVTGD 252

Qy 231 PKRPAVWLXWKGVPXRLPNLTRPCSGPRLPREARELRGOR 272
Db 253 PQDQ-----ITWK-----RKNPEMPVTRAVIAKDNRGRIER 284

RESULT 4
US-09-540-245A-16
; Sequence 16, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1381
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-16

Query Match 23.4%; Score 345; DB 3; Length 1381;
Best Local Similarity 33.7%; Pred. No. 9.6e-26;
Matches 91; Conservative 31; Mismatches 102; Indels 46; Gaps 8;

Qy 5 PQILVHPDQQLFQCGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 64
Db 4 PRIIEHPMDITVPKNDPFTFCNQAEQNPTFTIQWFKDGRKLTDTGSHRIMLPAGGLPFL 63

Qy 65 QPPARGHAHDGQALSTDLGVYTCESNRNLGTAVSRGARLSVAVLRDFOIQPRDMVAVG 124
Db 64 KV-----IHSRR--ESDAGTYWCEAKNEFGVARSNATLQVAVLRDEFERLEPANTRVAQ 116

Qy 125 EQFTLECGPPWGHPEPTVSWKDGKPLALQGR--HTVSGSLLMARAEKSDEXTYMCVA 182
Db 117 EVALMECCAPRGSPPEQISWRKNGQTLNLVGNKRIRIVDGNLAIQARQSDDDGRYQCVV 176

Qy 183 TNSAGHRESRAARVS-----IQEPQDYTEPVELLAV-----RIQLENVTLNPDPAEGPK 232
Db 177 KVVVGTRESATAFLKVVHRPFLIRGPQNTAVGVSSVVFQCR-----GGD 222

Qy 233 PRPAVWLXWKGVPXRLPNLTRPCSGPRLP 262
Db 223 PLPDV--LWR-----RTASGGNMP 239
```

```
RESULT 5
US-08-752-307B-14
; Sequence 14, Application US/08752307B
; Patent No. 5952171
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.307B
; FILING DATE: 19-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/020001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 630 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-752-307B-14

Query Match 17.0%; Score 251; DB 2; Length 630;
Best Local Similarity 34.5%; Pred. No. 8.9e-17;
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 5 PQILVHPQDOLFQGP-PAVMSCRASGPPPTIRWLLNGOPLSMVPPDPHLLPDGTL 63
Db 355 PYWLDEPN-LILAPGEDGRLVCRANGPKPSIQWLVNGEPIEGSPNPSREVAGDTI 413
Qy 64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQR 117
Db 414 -----RDTQIGSS--AVYQCNASNEHGVL--ANAFVSVL----DVPPI LAPRN 455
Qy 118 DMVAVVGQFT-LECGPWHGPEPTVSWKDGKPLALQPGHRTV-SGGSLLMARAEK 175
Db 456 QLIKVIQYNRTRLDC-PFFGSPITLRFKNGQGNMLDGGNYKAHENGSLMSMARKED 514
Qy 176 XYTCMVATNSAGHSRAARVSIQEP 201
Db 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

RESULT 6
US-09-707-802-14
; Sequence 14, Application US/09707802
; Patent No. 6391586
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
```

```
; Gearing, David P.
; Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/707.802
; FILING DATE: 07-No. 6391586-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/752.307
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/020001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 630 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-707-802-14

Query Match 17.0%; Score 251; DB 4; Length 630;
Best Local Similarity 34.5%; Pred. No. 8.9e-17;
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

Qy 5 PQILVHPQDOLFQGP-PAVMSCRASGPPPTIRWLLNGOPLSMVPPDPHLLPDGTL 63
Db 355 PYWLDEPN-LILAPGEDGRLVCRANGPKPSIQWLVNGEPIEGSPNPSREVAGDTI 413
Qy 64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQR 117
Db 414 -----RDTQIGSS--AVYQCNASNEHGVL--ANAFVSVL----DVPPI LAPRN 455
Qy 118 DMVAVVGQFT-LECGPWHGPEPTVSWKDGKPLALQPGHRTV-SGGSLLMARAEK 175
Db 456 QLIKVIQYNRTRLDC-PFFGSPITLRFKNGQGNMLDGGNYKAHENGSLMSMARKED 514
Qy 176 XYTCMVATNSAGHSRAARVSIQEP 201
Db 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

RESULT 7
US-09-991-326-14
; Sequence 14, Application US/09991326
; Patent No. 6395872
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; Gearing, David P.
; Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: US  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/991.326  
;; FILING DATE: 21-NOV-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/752.307  
;; FILING DATE: 19-NOV-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meiklejohn, Ph.D., Anita L.  
;; REGISTRATION NUMBER: 35,283  
;; REFERENCE/DOCKET NUMBER: 09404/020002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-542-5070  
;; TELEFAX: 617-542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 630 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-991-326-14  
  
Query Match 17.0%; Score 251; DB 4; Length 630;  
Best Local Similarity 34.5%; Pred. No. 8.9e-17;  
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;  
  
QY 5 PQILVHPDQQLFQPGP-PARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGILL 63  
Db 355 PYWLDEPQN-LILAFGEDRLVCRRNGNPKPSIQWLVNGEPIEGSPNPSREVAGDTIVF 413  
QY 64 LQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQR- 117  
Db 414 -----RTQIGSS--AVTQCNASNEHGILL---ANAFVSL----DVPPRLAPRN 455  
QY 118 DMVAVVGQFT-LEGCPWPWGHPPTVSWKDGKPLALQPGRHTV-SGSLLMARAEKSDS 175  
Db 456 QLIRKVIQYNRTRLDG-PFPGSPITPLRWFKNGQGNMLDGNYKAHENGSLMSMARKEDQ 514  
QY 176 XYMCVATNSAGHRESRAARVSIQEP 201  
Db 515 GIYTCVATNILGKVEAQ-VRLVKDP 539  
  
RESULT 8  
US-08-752-307B-12  
; Sequence 12, Application US/08752307B  
; Patent No. 5952171  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Gearing, David P.  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US

;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/752.307B  
;; FILING DATE: 19-NOV-1996  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meiklejohn, Ph.D., Anita L.  
;; REGISTRATION NUMBER: 35,283  
;; REFERENCE/DOCKET NUMBER: 09404/020001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-542-5070  
;; TELEFAX: 617-542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 607 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-752-307B-12  
  
Query Match 15.5%; Score 228; DB 2; Length 607;  
Best Local Similarity 29.5%; Pred. No. 1.7e-14;  
Matches 79; Conservative 38; Mismatches 99; Indels 52; Gaps 13;  
  
QY 1 QDSPPQILVHPDQQLFQPGP-PARMSCRASQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
Db 40 EDQPLSVL-EPEESTEE---QVLLACRARASPPATYRWKNGKTEMKLEPGSRHQLV-GGN 94  
QY 61 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQRDMV 120  
Db 95 LVIMNP-----TKAQDAGVYQCLASNPVGTVVSRRAILRFGFLQE-FSKEEDPV 143  
QY 121 -AVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL-QPGRHTVS--GGSLLMARAEKSDX 176  
Db 144 KAHEGNGWMLPCNPAPHYPGLSYRWLLNEFPNFIPTDGRHFVSTQTTGNLVIARTNASDLG 203  
QY 177 TYMCVATNSAGHRE-----SRAARVSIQ-----EPQDYTEPVELLAVRIQLE 218  
Db 204 NYSCLATS---HMDFTSKVSFKFAQLNLAEDTRLFAPSIRKARFPAETVALVQGVQVTL 260  
QY 219 NVTLAPDPAEGPKPRPAVWLXN-KVSG 245  
Db 261 CFAFGNPVPR-----IKWRKVDG 278  
  
RESULT 9  
US-09-707-802-12  
; Sequence 12, Application US/09707802  
; Patent No. 6391586  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Gearing, David P.  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/707,802  
FILING DATE: 07-NOV-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752,307  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 09404/020001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 607 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-707-802-12

Query Match 15.5%; Score 228; DB 4; Length 607;  
Best Local Similarity 29.5%; Pred. No. 1.7e-14;  
Matches 79; Conservative 38; Mismatches 99; Indels 52; Gaps 13;  
QY 1 QDSPPOILVHPDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
DB 40 EDQPLSVL-FPEESTEE---QVLLACRARASPPATYRWKMGTEMKLEPGSRHQLV-GGN 94  
QY 61 LLLQPPARGHAHDQALSTDLGVYTCASNRLGTAVSARGARLSVAVLRDFQIQPRDMV 120  
DB 95 LVIMNP-----TKAQDAGVYQCLASNPVGTWVSREAILRFGFLQE-FSKERDPV 143  
QY 121 -AVVGEQFTLEGCPGWGHEPTVSMWKGKPLAL-QPGRHTVS---GGSLLMARAEKSDX 176  
DB 144 KAHEGWVLPNCNPPAHYPGLSYRWLLNEFPNFIPTDGRHFVSQTGNLYIARTNASDLG 203  
QY 177 TYMCVATNSAGHRE-----SRAARVSIQ-----EPQDYTPVELLAVRIQLE 218  
DB 204 NYSCSLATS---HMDSTKSVFSKPAQLNLAEDTRLFAPSIKARPPAETVALVGQQTILE 260  
QY 219 NVTLLNPDPAEGPKRPAVWLXW-KVSG 245  
DB 261 CFAFGNPVPR-----IKWRKVDG 278

RESULT 10  
US-09-991-326-12  
Sequence 12, Application US/09991326  
Patent No. 6395872  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
Gearing, David P.  
Levinson, Douglas A.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/991,326  
FILING DATE: 21-NOV-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752,307  
FILING DATE: 19-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 09404/020002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 607 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-991-326-12  
Query Match 15.5%; Score 228; DB 4; Length 607;  
Best Local Similarity 29.5%; Pred. No. 1.7e-14;  
Matches 79; Conservative 38; Mismatches 99; Indels 52; Gaps 13;  
QY 1 QDSPPOILVHPDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
DB 40 EDQPLSVL-FPEESTEE---QVLLACRARASPPATYRWKMGTEMKLEPGSRHQLV-GGN 94  
QY 61 LLLQPPARGHAHDQALSTDLGVYTCASNRLGTAVSARGARLSVAVLRDFQIQPRDMV 120  
DB 95 LVIMNP-----TKAQDAGVYQCLASNPVGTWVSREAILRFGFLQE-FSKERDPV 143  
QY 121 -AVVGEQFTLEGCPGWGHEPTVSMWKGKPLAL-QPGRHTVS---GGSLLMARAEKSDX 176  
DB 144 KAHEGWVLPNCNPPAHYPGLSYRWLLNEFPNFIPTDGRHFVSQTGNLYIARTNASDLG 203  
QY 177 TYMCVATNSAGHRE-----SRAARVSIQ-----EPQDYTPVELLAVRIQLE 218  
DB 204 NYSCSLATS---HMDSTKSVFSKPAQLNLAEDTRLFAPSIKARPPAETVALVGQQTILE 260  
QY 219 NVTLLNPDPAEGPKRPAVWLXW-KVSG 245  
DB 261 CFAFGNPVPR-----IKWRKVDG 278

RESULT 11  
US-08-752-307B-13  
Sequence 13, Application US/08752307B  
Patent No. 5952171  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
Gearing, David P.  
Levinson, Douglas A.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752.307B  
FILING DATE: 19-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 09404/020001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-752-307B-13

Query Match 14.8%; Score 219; DB 2; Length 596;  
Best Local Similarity 28.2%; Pred. No. 1.4e-13;  
Matches 80; Conservative 39; Mismatches 119; Indels 46; Gaps 12;  
QY 5 PQILVHPDQQLFQGGPAR---MSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 61  
DB 25 PVFVKEPSNIFPVGSEDKITLNCARGNPSPHYRWQLNGSDID-TSLDHYRYKLNGNL 83  
QY 62 LLLQPPARGHAHDGQALSTDLGVYTCEASNLGTAVSRGARLSVAVLREDFOIQPRDWA 121  
DB 84 IVINPNR-----NWDTSYQCFATNSLGTIVSREAKLQFAYL-ENFKSRMRGRVS 132  
QY 122 V-VGEQFTLECGPPWGHPEPTVSW-WKDGKPLALQPGRHVTS--GGSLLMARAEKSDEXT 177  
DB 133 VREGGVLLCGPPHSGELSYAVWFNEYPSFVEEDSRFRVSQETGHLIYIAKVEPSDVGN 192  
QY 178 YMCVATN-----SAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENV 220  
DB 193 YTCVVTSTVNARVLGSPFTLVLRSDGVMGEYEPKLEQFPE--TLPA-ARGSTVKLECF 249  
QY 221 TLLNPD-----AEGKPRPAVWLXWKVSGPXRLNLTRECSG 258  
DB 250 ALGNPVPQINWRRSDG-MPFTTKIKLRFNGVLEIPNFQEDTG 292

RESULT 12  
US-09-707-802-13  
Sequence 13, Application US/09707802  
Patent No. 6391586  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
Gearing, David P.  
Levinson, Douglas A.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/991.326

APPLICATION NUMBER: US/09/707,802  
FILING DATE: 07-No. 6391586-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752,307  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 09404/020001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-707-802-13

Query Match 14.8%; Score 219; DB 4; Length 596;  
Best Local Similarity 28.2%; Pred. No. 1.4e-13;  
Matches 80; Conservative 39; Mismatches 119; Indels 46; Gaps 12;  
QY 5 PQILVHPDQQLFQGGPAR---MSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGTL 61  
DB 25 PVFVKEPSNIFPVGSEDKITLNCARGNPSPHYRWQLNGSDID-TSLDHYRYKLNGNL 83  
QY 62 LLLQPPARGHAHDGQALSTDLGVYTCEASNLGTAVSRGARLSVAVLREDFOIQPRDWA 121  
DB 84 IVINPNR-----NWDTSYQCFATNSLGTIVSREAKLQFAYL-ENFKSRMRGRVS 132  
QY 122 V-VGEQFTLECGPPWGHPEPTVSW-WKDGKPLALQPGRHVTS--GGSLLMARAEKSDEXT 177  
DB 133 VREGGVLLCGPPHSGELSYAVWFNEYPSFVEEDSRFRVSQETGHLIYIAKVEPSDVGN 192  
QY 178 YMCVATN-----SAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENV 220  
DB 193 YTCVVTSTVNARVLGSPFTLVLRSDGVMGEYEPKLEQFPE--TLPA-ARGSTVKLECF 249  
QY 221 TLLNPD-----AEGKPRPAVWLXWKVSGPXRLNLTRECSG 258  
DB 250 ALGNPVPQINWRRSDG-MPFTTKIKLRFNGVLEIPNFQEDTG 292

RESULT 13  
US-09-991-326-13  
Sequence 13, Application US/09991326  
Patent No. 6395872  
GENERAL INFORMATION:  
APPLICANT: McCarthy, Sean A.  
Gearing, David P.  
Levinson, Douglas A.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/991.326

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; APPLICATION NUMBER: 08/130,570
; FILING DATE: 01-OCT-1993
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-464-3
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; Query Match 14.8%; Score 218.5; DB 2; Length 1501;
; Best Local Similarity 30.9%; Pred. No. 5.6e-13;

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QY	57	PDGTLLLLOPPARGHAHDGOALST--DLGYVTCEASNRLGTAVSRGARLSVAIVT							
	:	: :::	:	:	:	:	:	:	:
Db	86	SSGAVLRIQP-----LRTPRDENVYECVAQNSVG-EITVHAKLT-VI							
QY	115	QRDMVAVVEGEF-----TLECGPPHGHPPTVSNWKGKPL--ALQFGG							
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Db	131	PPGFNIDMGPOLKWVERTRTATMLCAAS-GNPDPETITPKDFLPDVPDSASNGI							
QY	163	GSLIMARAEEKSDXTVMCVATNSAGHRESRAARVSIIQ 199							
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RESULT 15  
US-08-716-679-3  
; Sequence 3, Application US/08716679  
; Patent No. 5846800  
; GENERAL INFORMATION:  
; APPLICANT: Schlessinger, Joseph  
; APPLICANT: Yan, Hai  
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN  
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/716,679  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/130,570  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7683-043  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090  
 ; TELEFAX: 212-869-8864/9741  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1501 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-716-679-3

Query Match 14.8%; Score 218.5; DB 2; Length 1501;  
 Best Local Similarity 30.9%; Pred. No. 5.6e-13;  
 Matches 67; Conservative 37; Mismatches 74; Indels 39; Gaps 11;

Qy	2	DSPQILVHPDQLFQGGPARMSCRASGQPPPTIRM-----LNGQPLSMVPPDPHLL	56
Db	30	EEPRFIREPKDQIGVSGVASFVCATGDKPRVTWKKGKVSQRFETIDFDE----	85
Qy	57	PDGTLILLQPPARGHAHDQALST--DLGVYTCASNRLGTAVSRGARLSVAVLRDFOI	114
Db	86	SSGAVLRIQP-----LRTPRDENVYECVAQNSVG-EITVHAKLT--VLRED-QL	130
Qy	115	QPRDMVAVVGEQF-----TLECGPPMGHPPTVSWMKDGKPL--ALQGR-HTVSG	162
Db	131	PPGFNIDMGPLKXVVERTRTATMLCAAS-GNPDPEITWFKDFLPVDPASNGRIKQLRS	189
Qy	163	GSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQ	199
Db	190	GALQIESSEETDQGYECVATNSAGVRYSSPANLYVR	226

Search completed: January 30, 2004, 15:57:51  
 Job time : 13.8238 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 30, 2004, 15:54:49 ; Search time 28.1244 Seconds  
(without alignments)  
2039.494 Million cell updates/sec

Title: US-10-047-021-86\_COPY\_28\_303

Perfect score: 1475

Sequence: 1 QDSPPQILVHPDQLFQCG.....SGPRLPREARELRGQRNTG 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1469	99.6	303	12	US-10-047-021-86
2	1469	99.6	304	12	Sequence 86, Appl
3	1311	88.9	480	11	US-10-411-224-86
4	1311	88.9	385	10	US-09-786-753-158
5	1311	88.9	985	10	US-09-978-295A-211
6	1311	88.9	985	10	US-09-978-697-211
7	1311	88.9	985	10	US-09-978-192A-211
8	1311	88.9	985	10	US-09-999-832A-211
9	1311	88.9	985	11	US-09-978-189-211
10	1311	88.9	985	11	US-09-978-608A-211
11	1311	88.9	985	11	US-09-978-585A-211
12	1311	88.9	985	11	US-09-978-191A-211
13	1311	88.9	985	11	US-09-978-403A-211
14	1311	88.9	985	11	US-09-978-564A-211
15	1311	88.9	985	11	US-09-999-833A-211
					US-09-981-915A-211

16	1311	88.9	985	11	US-09-978-824-211
17	1311	88.9	985	11	US-09-918-585A-211
18	1311	88.9	985	11	US-09-978-423A-211
19	1311	88.9	985	11	US-09-978-193A-211
20	1311	88.9	985	11	US-09-999-830A-211
21	1311	88.9	985	11	US-09-978-757A-211
22	1311	88.9	985	11	US-09-978-187B-211
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25	1311	88.9	985	12	US-09-978-188A-211
26	1311	88.9	985	12	US-09-978-298A-211
27	1311	88.9	985	12	US-10-143-031A-211
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44	1311	88.9	985	12	US-09-978-681A-211
45	1311	88.9	985	12	US-09-999-829A-211

ALIGNMENTS

RESULT 1  
US-10-047-021-86  
; Sequence 86, Application US/10047021  
; Publication No. US20040002591A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 50 Human Secreted Proteins  
; FILE REFERENCE: P2016P2  
; CURRENT APPLICATION NUMBER: US/10/047,021  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: US 60/262,066  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 09/722,329  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/262,109  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: PCT/US98/18360  
; PRIOR FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: US 60/057,626  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/057,663  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/057,669  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/058,667  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: US 60/058,974  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: US 60/058,973  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: US 60/058,666  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: US 60/090,112  
; PRIOR FILING DATE: 1998-06-22  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 303

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86

Query Match          99.6%; Score 1469; DB 12; Length 303;
Best Local Similarity 100.0%; Pred. No. 7.2e-114;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 60
DB 28 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 87
QY 61 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 120
DB 88 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 147
QY 121 AVVGEQFTLECGPWGHPPTVSMWKDGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 180
DB 148 AVVGEQFTLECGPWGHPPTVSMWKDGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 207
QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 240
DB 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 267
QY 241 WKVSGPXRLPNLTRPCSGPRLPREARELRGQRNTG 276
DB 268 WKVSGPXRLPNLTRPCSGPRLPREARELRGQRNTG 303

RESULT 2
US-10-411-224-86
; Sequence 86, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 304

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-411-224-86

Query Match          99.6%; Score 1469; DB 12; Length 304;
Best Local Similarity 100.0%; Pred. No. 7.2e-114;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 60
DB 28 QDSPPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQLPSMVPPDPHLLPDGT 87
QY 61 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 120
DB 88 LLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 147
QY 121 AVVGEQFTLECGPWGHPPTVSMWKDGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 180
DB 148 AVVGEQFTLECGPWGHPPTVSMWKDGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 207
QY 181 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 240
DB 208 VATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPVAVWLX 267
QY 241 WKVSGPXRLPNLTRPCSGPRLPREARELRGQRNTG 276
DB 268 WKVSGPXRLPNLTRPCSGPRLPREARELRGQRNTG 303

RESULT 3
US-09-796-753-158
; Sequence 158, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
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; PRIOR FILING DATE: 1999-06-29
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;; PRIOR APPLICATION NUMBER: 09/345,464  
;; PRIOR FILING DATE: 1999-06-30  
;; PRIOR APPLICATION NUMBER: 09/365,164  
;; PRIOR FILING DATE: 1999-07-30  
;; PRIOR APPLICATION NUMBER: 09/399,723  
;; PRIOR FILING DATE: 1999-09-20  
;; PRIOR APPLICATION NUMBER: 09/409,634  
;; PRIOR FILING DATE: 1999-09-30  
;; PRIOR APPLICATION NUMBER: 09/471,179  
;; PRIOR FILING DATE: 1999-12-23  
;; PRIOR APPLICATION NUMBER: 09/474,071  
;; PRIOR FILING DATE: 1999-12-29  
;; PRIOR APPLICATION NUMBER: 09/474,072  
;; PRIOR FILING DATE: 1999-12-29  
;; PRIOR APPLICATION NUMBER: 09/514,010  
;; PRIOR FILING DATE: 2000-02-25  
;; PRIOR APPLICATION NUMBER: 09/516,745  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 09/572,002  
;; PRIOR FILING DATE: 2000-05-14  
;; PRIOR APPLICATION NUMBER: 09/597,993  
;; PRIOR FILING DATE: 2000-06-19  
;; PRIOR APPLICATION NUMBER: 09/599,596  
;; PRIOR FILING DATE: 2000-06-22  
;; PRIOR APPLICATION NUMBER: 09/630,334  
;; PRIOR FILING DATE: 2000-07-31  
;; PRIOR APPLICATION NUMBER: 09/606,565  
;; PRIOR FILING DATE: 2000-06-29  
;; PRIOR APPLICATION NUMBER: 09/606,317  
;; PRIOR FILING DATE: 2000-06-29  
;; PRIOR APPLICATION NUMBER: 09/665,666  
;; PRIOR FILING DATE: 2000-09-20  
;; PRIOR APPLICATION NUMBER: 09/677,751  
;; PRIOR FILING DATE: 2000-09-30  
;; NUMBER OF SEQ ID NOS: 162  
;; SEQ ID NO 158  
;; LENGTH: 480  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-796-753-158

Query Match 88.9%; Score 1311; DB 11; Length 480;  
Best Local Similarity 98.8%; Pred. No. 1.6e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 QDSPPQILVHPDQLFQGGPARMSCRASGQPPTIRLLNGQPLSMVPPDPHLLPDGT 60  
DB 59 QDSPPQILVHPDQLFQGGPARMSCRASGQPPTIRLLNGQPLSMVPPDPHLLPDGT 118  
QY 61 LLLQPPARGHAHDGQALSTDLGVVTCBASNRLGTAVSRGARLSVAVLRDPFIQIPDMV 120  
DB 119 LLLQPPARGHAHDGQALSTDLGVVTCBASNRLGTAVSRGARLSVAVLRDPFIQIPDMV 178  
QY 121 AVVGQFTLECGPPNGHPPTVSWWKGKPLALQPGRTVSGSLLMARAEKSDXTYMC 180  
DB 179 AVVGQFTLECGPPNGHPPTVSWWKGKPLALQPGRTVSGSLLMARAEKSDGTMYC 238  
QY 181 VATNSAGHRESRAARVSTQEPDYTEPVELLAVRIQLENVTLLNPDPAEGKPPRAVWLX 240  
DB 239 VATNSAGHRESRAARVSTQEPDYTEPVELLAVRIQLENVTLLNPDPAEGKPPRAVWLS 298  
QY 241 WKVSGP 246  
DB 299 WKVSGP 304

RESULT 4  
US-09-978-295A-211  
; Sequence 211. Application US/09978295A  
; Patent No. US2002015606A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.

;; APPLICANT: Botstein, David  
;; APPLICANT: Deanoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kllavin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James;  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: ROY, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C11  
;; CURRENT APPLICATION NUMBER: US/09/978,295A  
;; CURRENT FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/064249  
;; PRIOR FILING DATE: 1997-11-03  
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;; PRIOR FILING DATE: 1997-11-13  
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;; PRIOR FILING DATE: 1998-03-13  
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 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 60/079923  
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 ; PRIOR FILING DATE: 1998-04-22  
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 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 10; Length 985;

Best Local Similarity 98.8%; Fred. No. 3.7e-100; Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	QDSPPQILVHPQDLFOGPGPARMSCRASGPPPTIRWLLNQPLSWVPPDPHLLPDGT	60
Db	6	QDSPPQILVHPQDLFOGPGPARMSCRASGPPPTIRWLLNQPLSWVPPDPHLLPDGT	65
Qy	61	LLLLQPPARGHADGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV	120
Db	66	LLLLQPPARGHADGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDMV	125
Qy	121	AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALOPGHTVSGSLLMARAEKSDXTYMC	180
Db	126	AVVGEQFTLECGPPWGHPEPTVSWKDGKPLALOPGHTVSGSLLMARAEKSDXTYMC	185
Qy	181	VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENTVTLNPDPAEGPKPPAVWLX	240
Db	186	VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENTVTLNPDPAEGPKPPAVWLX	245
Qy	241	WKVSGP	246
Db	246	WKVSGP	251

RESULT 5  
US-09-978-697-211  
; Sequence 211: Application US/09978697  
; Patent No. US20020165284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 10; Length 985;  
Best Local Similarity 98.8%; Pred. No. 3.7e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 QDSPPQILVHQQDQLFQGGPARGMCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
Db 6 QDSPPQILVHQQDQLFQGGPARGMCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 65  
Qy 61 LLLQPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGRLSVAVLRDFOQPRDMV 120  
Db 66 LLLQPPARGHAHQDQALSTDLGVYTCEASNRGLGTAVSRGRLSVAVLRDFOQPRDMV 125  
Qy 121 AVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 180

Db 126 AVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHVTSGSLLMARAEKSDXTYMC 185  
Qy 181 VATNSAGHRESRAARVSIQEPQDYTFEPVELLAVRIQLENTVTLNPOPAEGPKRPAVWLX 240  
Db 186 VATNSAGHRESRAARVSIQEPQDYTFEPVELLAVRIQLENTVTLNPOPAEGPKRPAVWLX 245  
Qy 241 WKVSGP 246  
Db 246 WKVSGP 251

## RESULT 6

US-09-378-192A-211  
Sequence 211, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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Query Match 88.9%; Score 1311; DB 10; Length 985;  
Best Local Similarity 98.8%; Pred. No. 3.7e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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Db 126 AVVGQFTLECGPPMGHPPTVSMWKGKPLALQFGRHTVSGGSLLMARAEKSDEXTVMC 185  
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Db 186 VATSAGHRESRAARVSIQEQDYTEPVELLAVRIQLENNVLLNPDPAEGPKPPAVWLS 245  
Qy 241 WKVSGP 246  
Db 246 WKVSGP 251

## RESULT 7

US-09-999-832A-211

; Sequence 211, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvarcoff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
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; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PLC63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
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; PRIOR APPLICATION NUMBER: 60/085697  
  
Query Match 88.9%; Score 1311; DB 10; Length 985;  
Best Local Similarity 98.8%; Pred. No. 3.7e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 QDSPQILVHPQDQLFQGGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 60  
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6 QDSPQILVHPQDQLFQGGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDGT 65  
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186 VATNSAGHRESRAARVSIQEPQDYTPVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 245  
Qy 241 WKVSGP 246  
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246 WKVSGP 251

RESULT 8

US-09-978-189-211  
; Sequence 211, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
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; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/081919  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 88.9%; Score 1311; DB 11; Length 985;  
Best Local Similarity 98.8%; Pred. No. 3.7e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 6 QDSPPQILVHPQDQLFOGPGPARMSCRASQGPPTIRMLLNGQPLSMVPPDPHLLPDGT 65  
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DB 66 LLLLQPPARGHAHQALSTDLGVVTCASNRLGTAVSRGARLSVAVLRDFQIQPRDMV 125  
QY 121 AVVGEQFTLECGPPGHPPEPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 180  
DB 126 AVVGEQFTLECGPPGHPPEPTVSWKDGKPLALQPGRHTVSGSLLMARAESDXTYMC 185  
QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240  
DB 186 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 245  
QY 241 WKVSGP 246  
DB 246 WKVSGP 251

## RESULT 9

US-09-978-608A-211  
; Sequence 211, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC22

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; CURRENT APPLICATION NUMBER: US/09/978.608A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; SEQ ID NO 211  
; LENGTH: 985  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-608A-211

Query Match 88.9%; Score 1311; DB 11; Length 985;  
Best Local Similarity 98.8%; Pred. No. 3.7e-100;  
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDSPPQILVHPQDQLFOGPGPARMSCRASQGPPTIRMLLNGQPLSMVPPDPHLLPDGT 60  
DB 6 QDSPPQILVHPQDQLFOGPGPARMSCRASQGPPTIRMLLNGQPLSMVPPDPHLLPDGT 65  
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QY 181 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 240  
DB 186 VATNSAGHRESRAARVSIQEPDYTEPVVELLAVRIQLENVTLNPDPAEGPKPRPAVWLX 245  
QY 241 WKVSGP 246  
DB 246 WKVSGP 251

## RESULT 10

US-09-978-585A-211  
; Sequence 211, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC15  
; CURRENT APPLICATION NUMBER: US/09/978.585A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624

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; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 211
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-211

Query Match      88.9%; Score 1311; DB 11; Length 985;
Best Local Similarity 98.8%; Pred. No. 3.7e-100;
Matches 243; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDSPQLVHPDQDLFQGGPARMSCRASGQPPPTIRWLNQGLSMVPPDPHLLPDGT 60
Db 6 QDSPQLVHPDQDLFQGGPARMSCRASGQPPPTIRWLNQGLSMVPPDPHLLPDGT 65

Qy 61 LLLQPPARGHAHQALSTDLGVYTCASNRLGTAVSRGARLSAVLREDFQIQPRDMV 120
Db 66 LLLQPPARGHAHQALSTDLGVYTCASNRLGTAVSRGARLSAVLREDFQIQPRDMV 125

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Db 126 AVGEQFTLEGCPWGHPEPTVSWKDGKPLALQGRHTVSGSLLMARAEKSDGTYMC 185

Qy 181 VATNSAGHRESRAARVSIQEPQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPAYWLX 240
Db 186 VATNSAGHRESRAARVSIQEPQDYTEPVVELLAVRIQLENVTLNPDPAEGPKRPAYWLS 245

Qy 241 WKVSGP 246
Db 246 WKVSGP 251

RESULT 11
US-09-978-191A-211
; Sequence 211, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
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Qy	224	SerIleGlnclupProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGln	243
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Qy	244	LeuGluAsnValThrLeuLeuLeuLeuProAspProAlaGluGlyProIlyProArgProAla	263
Db	721	CTGGAATAATGTGACATGCTGTGAACCGGATCCTGCGAGAGGGCCCAAGCTAGACCGCG	780
Qy	264	ValTrpLeu***TrpIysValSerGlyPro***-ArgLeuProAsnLeuThrArgProCys	283
Db	781	GTGTGGCTCAGCTGGGAAGGTCAAGTGGCCCTGCTGGCGCCTGCCTCAATCTTACACGGCCTTG	840
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Db	841	TTCAGGACCCAGACTCCCTCCCGGGAGGCCAGGGAGCTCCCTGGGGCGAGGG	889
RESULT 5			
US-09-978-697-210			
; Sequence 210, Application US/09978697			
; Patent No. US20020169284A1			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Baker Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan			
; APPLICANT: Ferrara, Napoleon			
; APPLICANT: Flivaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
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; APPLICANT: Grimaldi, J. Christopher			
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; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Shelton, David L.			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; FILE REFERENCE: P2630P1C27			
; CURRENT APPLICATION NUMBER: US/09/978,697			
; CURRENT FILING DATE: 2001-10-16			
; PRIOR APPLICATION NUMBER: 09/918595			
; PRIOR FILING DATE: 2001-07-30			
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;; PRIOR APPLICATION NUMBER: 60/085338  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085323  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2.9e-136 Length: 3716  
Score: 1550.00 Matches: 292  
Percent Similarity: 98.65% Conservative: 1  
Best Local Similarity: 98.32% Mismatches: 3  
Query Match: 96.39% Indels: 1  
DB: 10 Gaps: 0

US-10-047-021-86 (1-303) x US-09-978-295A-210 (1-3716)

Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23  
Db 1 GGAGGAGACAGCCCTCTGGGGGCGAGGGTTCCTGCTGCTGCTGCTCATATG 60  
Qy 24 GlyGlyMetAlaGlnAspSerProGlnLeuValHisProGlnAspGlnLeuPhe 43  
Db 61 GGAGGATGGCTCAGGACTCCCGCCCGCAGATCTAGTCCACCCCGAGCCAGCTGTC 120  
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIle 63  
Db 121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCAAGCTCAGGCCAGCCACCTCCCACTC 180  
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83  
Db 181 CGCTGGTTCGTAATGGGACGCCCCCTGAGCATGGTGCCCGAGACCCACACCTCTCTG 240  
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103  
Db 241 CCTGATGGACCCCTCTGCTGCTACAGCCCTTCCCGGGGACATGCCACGATGCCAG 300  
Qy 104 AlaLeuSerThrAspLeuGlyValTrpThrCysGluAlaSerAsnArgLeuGlyThrAla 123  
Db 301 GCCCTGTCCAGACCTGGGTGTACACATGTGAGGCCAGCAACCGGCTTGGCAGCGCA 360  
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAppPheGlnIleGlnPro 143  
Db 361 GTCAGCAGAGCGCTCGGCTCTGTGCTGCTCTCCCGGAGGATTTCCAGATCCAGCT 420  
Qy 144 ArgAspMetValAlaValGlyGlnPheThrLeuGluCysGlyProProTrpGly 163  
Db 421 CGGACATGGTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
Qy 164 HisProGluProThrValSerTrpTrpAspGlyLysProLeuAlaLeuGlnProGly 183  
Db 481 CACCCAGAGCCACAGTCTCATGTGGAAAGATGGAAACCCCTGGCCCTCCAGCCCGGA 540





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Pred. No.: 1.23e-141 Length: 1346
Score: 1602.00 Matches: 303
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.63% Indels: 0
DB: 13 Gaps: 0

US-10-047-021-86 (1-303) x US-10-411-224-31 (1-1346)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
DB 31 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGGTTCCCTGCTCTGCTGCTG 90
QY 21 LeuileMetGlyGlyMetAlaGlnAspSerProProGlnleLeuValHisProGlnAsp 40
DB 91 CTCATCATGGAGGAGCATGGCTCAGACTCCCGCGCCCGAGATCTTAGTCCACCCCGAGGAC 150
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
DB 151 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTGGCGAGCTCTCAGGCCAGCCACT 210
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
DB 211 CCCACCATCCGCTGGTGTGTAATGGGAGCCCTGGAGCATGGTGGTCCCGAGACCCACAC 270
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
DB 271 CACTCTCTGCTGATGGGACCTTCTGTGCTACAGCCCTGCGCGGGAGCATGCCAC 330
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeu 120
DB 331 GATGCCAGGCCCTGTCCACAGACTGGTGTGTACATGATGGAGCCCGAGCAACCGGCTT 390
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
DB 391 GGCAGCGCAGTCCAGAGAGCCCTCGGCTGTCTGTGGCTGTCTCCGGAGGATTTCCAG 450
QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
DB 451 ATCCAGCTCGGAGCATGGTGTCTGTGGTGTGAGCATTTACTCTGGAATGTGGGCG 510
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
DB 511 CCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 570
QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
DB 571 CAGCCCGGAAGGCACACAGTGTCCGGGGGTCCTGCTGATGGCAAGAGCAGAGAAGAGT 630
QY 201 AspGlu**ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
DB 631 GACGANGGACCTCATGTGTGTGGCCACCAACAGCGAGGACACAGGAGAGCCGCCA 690
QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAlaVal 240
DB 691 GCCCGGTTTCCATCCAGGAGCCCGAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTG 750
QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuLeuAsnProAspProAlaGluGlyProLysPro 260
DB 751 CGAATTCAGCTGGAAATATGACACTCTGTAACCCCGGATCTCTGCAGAGGGGCCCAAGCCT 810
QY 261 ArgProAlaValTrpLeu**TrpLysValSerGlyPro**ArgLeuProAsnLeuThr 280
DB 811 AGACCGCGGTGTGCTCARTGGAAAGTCACTGGGCGCTTNTGGCGCTGCCCAATCTTACA 870
QY 281 ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
DB 871 CGGCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCGAGGAGG 930
QY 301 AsnThrGly 303
DB 931 AACACAGGA 939
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RESULT 3  
US-10-059-585-21  
; Sequence 21, Application US/10059585  
; Publication No. US20030082776A1  
; GENERAL INFORMATION:  
; APPLICANT: Ota, Toshio  
; APPLICANT: Isogai, Takao  
; APPLICANT: Nishikawa, Tetsuo  
; APPLICANT: Hayashi, Koji  
; APPLICANT: Otsuka, Kaoru  
; APPLICANT: Yamamoto, Jun-ichi  
; APPLICANT: Ishii, Shizuko  
; APPLICANT: Sugiyama, Tomoyasu  
; APPLICANT: Wakamatsu, Ai  
; APPLICANT: Nagai, Keiichi  
; APPLICANT: Otsuki, Tetsuji  
; APPLICANT: Funahashi, Shin-Ichi  
; APPLICANT: Senoo, Chiaki  
; APPLICANT: Nezu, Jun-Ichi  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN  
; FILE REFERENCE: 06501-098001  
; CURRENT APPLICATION NUMBER: US/10/059,585  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP00/05060  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 60/183,322  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: US 60/159,590  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: JP 2000-118776  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-183767  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: JP 11-248036  
; PRIOR FILING DATE: 1999-07-29  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 4262  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)...(2415)  
US-10-059-585-21

Alignment Scores:  
Pred. No.: 7.37e-137 Length: 4262  
Score: 1557.00 Matches: 294  
Percent Similarity: 98.33% Conservative: 1  
Best Local Similarity: 98.00% Mismatches: 4  
Query Match: 96.83% Indels: 1  
DB: 15 Gaps: 0

US-10-047-021-86 (1-303) x US-10-059-585-21 (1-4262)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20  
DB 40 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGGTTCCCTGCTCTGCTGCTG 99  
QY 21 LeuileMetGlyGlyMetAlaGlnAspSerProProGlnleLeuValHisProGlnAsp 40  
DB 100 CTCATCATGGAGGAGCATGGCTCAGACTCCCGCGCCCGAGATCTTAGTCCACCCCGAGGAC 159  
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
DB 160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGTGGCCAGGCTTCAGGCCAGCCACT 219  
QY 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80  
DB 220 CCCACCATCCGCTGGTGTGTAATGGGAGCCCTGGAGCATGGTGGTGGCCCGAGACCCAC 279

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; PRIOR APPLICATION NUMBER: US 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (637)..(637)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (850)..(850)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-047-021-31

Alignment Scores:
Pred. No.: 1,23e-141 Length: 1346
Score: 1602.00 Matches: 303
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.63% Indels: 0
DB: 12 Gaps: 0

US-10-047-021-86 (1-303) x US-10-047-021-31 (1-1346)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
Db 31 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGCGAGGGTTCCTCGCTCTGCTGCTCGT 90
Qy 21 LeulleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
Db 91 CTCATCATGGGAGGATGGCTCAGGACTCCCGGCCCGAGATCTTAGTCCACCCCGAGGAC 150
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
Db 151 CAGCTGTTCCAGGGCCCTTGGCCCTCCAGGATGAGCTCCGAGCCTCAGGCTCAGGCACCT 210
Qy 61 ProThrIleArgTTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
Db 211 CCCACCATCCGCTGTTGCTGAATGGGCGAGCCCTCGAGCATGGTGTGCCCGCCAGACCCAC 270
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
Db 271 CACCTCTCGCTGTAGTGGGACCTTCTGCTGTACAGCCCTCGCCCGGGGACATGCCAC 330
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrCysGluAlaSerAsnArgLeu 120
Db 331 GATGGCCAGGCCCTTCCAGACCTGGGTGTCTACACATGTGAGCCCGAGCACCGGGTT 390
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
Db 391 GGCAGCGGAGTCCAGAGGGGCTCGGCTGTCTGTGGTGTCTCTCGGGGAGATTTCAG 450
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
Db 451 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGTGGAGCAGTTTACTCTCGAAATGTGGCCG 510
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTTrpLysAspGlyLysProLeuAlaLeu 180
Db 511 CCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTTGGCCCTC 570
Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
Db 931 AACACAGGA 939

RESULT 2
US-10-411-224-31
; Sequence 31, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (637)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (850)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-411-224-31
Alignment Scores:
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GenCore version 5.1.6  
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Perfect score: 1608  
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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:
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- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-047-021-31  
; Sequence 31, Application US/10047021  
; Publication No. US20040002591A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 50 Human Secreted Proteins  
; FILE REFERENCE: P2016P2  
; CURRENT APPLICATION NUMBER: US/10/047,021  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: US 60/262,066  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 09/722,329  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/262,109  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: PCT/US98/18360  
; PRIOR FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: US 60/057,626  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/057,663  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/057,669  
; PRIOR FILING DATE: 1997-09-05

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3	1557	96.8	4262	15	US-10-059-585-21	Sequence 21, Appl
4	1550	96.4	3716	10	US-09-978-295A-210	Sequence 210, App
5	1550	96.4	3716	10	US-09-978-697-210	Sequence 210, App
6	1550	96.4	3716	10	US-09-978-192A-210	Sequence 210, App
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43	1550	96.4	3716	13	US-10-145-124A-210	Sequence 210, App
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45	1550	96.4	3716	13	US-10-165-247A-210	Sequence 210, App

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Job time : 83.4611 secs

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QY 278 -AbnLeuThrArgProCysSer-GlyPro-----ArgLeuProA 290  
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Db 960 TGCCTGGCGGAGAACTCACTGGGCAG 985  
RESULT 14  
US-09-638-649-2  
; Sequence 2, Application US/09638649  
; Patent No. 6563015  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED  
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 0575/62175  
; CURRENT APPLICATION NUMBER: US/09/638,649  
; CURRENT FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1426  
; TYPE: DNA  
; ORGANISM: Bos Taurus  
US-09-638-649-2  
Alignment Scores:  
Pred. No.: 1,026-07 Length: 1426  
Score: 199.00 Matches: 89  
Percent Similarity: 38.63% Conservative: 35  
Best Local Similarity: 27.73% Mismatches: 122  
Query Match: 12.38% Indels: 76  
DB: 4 Gaps: 17  
US-10-047-021-86 (1-303) x US-09-638-649-2 (1-1426)  
QY 32 ProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly---ProGlyProAlaArg 50  
Db 376 CCAGAAATT---GTTGATCTCGCTCTGCACTCATGGTGTGTCCTCCCAATAAGGTGGG 432  
QY 51 MetSerCysArgAlaSerGlyGlnProProProThrIleArgTrrpLeuLeuAsnGlyGln 70  
Db 433 ACATGTGTGTCGAGGGGGGTACCTCGACGGGACTCTTAACCTGCTCTTGGATGGGAA 492  
QY 71 ProLeuSerMetValProProAspProHisLeuLeuProAspGlyThrLeuLeuLeu 90  
Db 493 ACT-----CTGATTCCTGATGGCAAGAGGTGTCA 522  
QY 91 LeuGlnProProAlaArgGlyHisAlaHisAspGlyGln---AlaLeuSerThrAspLeu 109  
Db 523 GTGAAGGAAGAGACCAAGACAGACACCCAAAGACAGGGCTTTTCAGCTCCATTCCGAGGTG 582  
QY 110 GlyVal-----TyrThrCysGluAlaSer--- 117  
Db 583 ATGTGACCCAGCTCGGGGAGGAGCTCTCCACCCCACTTCTCTCTGTAGCTTCCACCCCT 642  
QY 118 -----AsnArgLeuGlyThrAlaVal----- 124  
Db 643 GGCCTTCCCGCGCGCGAGCCCTGCACACGGCCCGCCATCCAGCTCAGGCTGTGAGTGA 702  
QY 125 -----SerArgGlyAlaArgLeuSerValAlaValLeuArgGlu---AspPheGln 140

Db 703 CACCGAGTGGGGAGGGCCCCAACGTCGACGCTGTGCTCACTGAAGGAAGTCCAGTTGGTG 762  
QY 141 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 160  
Db 763 GTAGAGCCCAAGAGGGGAGGAGTAGCTCTCGTGGTGTACTGTGACCTGTGACCTGTGAAGCC 822  
QY 161 ProTrrpGlyHisProGluProThrValSerTrrpLysAspGlyLysProLeuAlaLeu 180  
Db 823 CCC---GCCCAGCCCCCACCCTCAATCCACTGGATCAAGGATGGCAGGCCCTCCCTCCCTT 879  
QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGlyLysSer 200  
Db 880 CCCCT-----GGCCCCATGCTGCTCTCTCCACAGAGTAGGGCCCTGAG 921  
QY 201 AspGlu\*\*\*ThrTyrMetCysValAlaThrAsn---SerAlaGlyHisArgGluSerArg 219  
Db 922 GACCAAGGAACCTACAGTTGTGTGGCCACCCTCCAGCCATCGGCCCCCAGGAGGCGCT 981  
QY 220 AlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuAla 239  
Db 982 GCTGTACGCTCAGCATCATCGAA-----ACAGCGAGGAGGGGACGACTGCA 1029  
QY 240 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259  
Db 1030 GGCTCTGTGGAAGGGCGGGCTGGAACCCCTAGC-CCTGACCCCTGGGGATCTCTGGGAGG 1088  
QY 260 Pro-----ArgProAlaValTrrp-----Leu\*\*\*TrrpLysValSer----- 271  
Db 1089 CTTGGGGACAGTCCCTCTGCTCATTTGGGGTCATGTTGGTCATCGAAGCGGCGCAACGCA 1148  
QY 272 -----GlyPro\*\*\*ArgLeu-----ProAsnLeuThr 280  
Db 1149 AGGACAGAGAGGAAGTCCCGGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1208  
QY 281 ArgProCysSerGlyProArgLeuProArgGlu-----AlaArgGluLeuArgGlyGln 298  
Db 1209 GAACCAAGCAGAGAGGCGCGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1268  
QY 299 Arg 299  
Db 1269 CGG 1271  
RESULT 15  
US-08-341-843B-1  
; Sequence 1, Application US/08341843B  
; Patent No. 5872225  
; GENERAL INFORMATION:  
; APPLICANT: Lemmon, Vance  
; TITLE OF INVENTION: A Method for Characterizing the  
; TITLE OF INVENTION: Nucleotide Sequence of LicAM and  
; Patent No. 5872225  
; TITLE OF INVENTION: the Nucleotide Sequence  
; TITLE OF INVENTION: Characterized Thereby  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
; ADDRESSEE: Minnich & McKee  
; STREET: 1100 Superior Avenue  
; STREET: Suite 700  
; CITY: Cleveland  
; STATE: Ohio  
; COUNTRY: U.S.A.  
; ZIP: 44114-2518  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; MEDIUM TYPE: storable  
; COMPUTER: Compaq Prolinea 5100e  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/341,843B  
; FILING DATE: No. 5872225ember 18, 1994



Db 550 TGCAGT---ACCATGGGGAATCCAAACACGAGCCATTTTCATGGTTCAAGATGAAACTGCA 606  
Qy 178 LeuAlaLeu---GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArg 196  
Db 607 CTGAAAATGACAGAGCTCGAAGCTTCTGCTTGTAGTCTGGGAATTAAGAATTGCAAT 666  
Qy 197 AlaGluLeuSerAspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArg 216  
Db 667 GTTCAGCTTGAAGATGACGAGAAATATCGATGTTTGGCAAGAAACAGCCTGGGCTTCGAG 726  
Qy 217 GluSerArgAlaAlaArgValSerIleGln 226  
Db 727 TATTCAGATCTGGGCTCTGGAAGTGCAG 756

## RESULT 13

US-08-427-497E-6  
Sequence 6, Application US/08427497E  
Patent No. 5969124  
GENERAL INFORMATION:  
APPLICANT: Lemmon, Vance  
TITLE OF INVENTION: A Method for Characterizing the  
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and  
Patent No. 5969124  
TITLE OF INVENTION: the Nucleotide Sequence  
TITLE OF INVENTION: Characterized Thereby  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
MEDIUM TYPE: storable  
COMPUTER: Compaq Prolinea 5100e  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/427,497E  
FILING DATE: April 24, 1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/904,991  
FILING DATE: June 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175  
REFERENCE/DOCKET NUMBER: CWR 2 149-3-1  
TELEPHONE: (216) 861-5582  
TELEFAX: (216) 241-1666  
TELEX: (216) 980162  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1042  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: nucleic acids  
HYPOTHETICAL: irrelevant  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: homo sapiens  
INDIVIDUAL ISOLATE: 17-18 week fetus  
IMMEDIATE SOURCE:  
LIBRARY: Stratagene cDNA Library 936206  
CLONE: C2  
PUBLICATION INFORMATION:  
AUTHORS: Hlavin, Mary Louise

AUTHORS: Lemmon, Vance  
TITLE: Molecular structure and functional testing of  
human L1CAM: an interspecies comparison.  
JOURNAL: GENOMICS  
VOLUME: 11  
ISSUE:  
PAGES: 416-423  
DATE: 1991  
RELEVANT RESIDUES IN SEQ ID NO: -26 to 1016  
US-08-427-497E-6

Alignment Scores:  
Pred. No.: 6,84e-08 Length: 1042  
Score: 199.00 Matches: 88  
Percent Similarity: 26.67% Conservative: 33  
Best Local Similarity: 26.67% Mismatches: 107  
Query Match: 12.38% Indels: 102  
DB: 2 Gaps: 19

US-10-047-021-86 (1-303) x US-08-427-497E-6 (1-1042)

Qy 26 MetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly 45  
Db 135 ATCAGGAAACAGTCTCCACGGCGCTGTTGTTCTTCCCCACAGATGACATC  
Qy 46 ProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThrIleArgTrp 65  
Db 186 -----AGCCTCAAGTGTAGCCAGTGCAGCCCGGAGAGTGCAGTCCGCTGG 233  
Qy 66 LeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuProAsp 85  
Db 234 ACGAGGGATGTGTC-----CACTTCAAAACCCCAAG 263  
Qy 86 GlyThrLeu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103  
Db 264 GAAGAGCTGGGTGTACCGTGTACCGTGTACCGTGTACCGTGTACCGTGTACCGTGTAC 308  
Qy 104 AlaLeuSerThrAsp-----LeuGlyValTyrThrCys 114  
Db 309 TTCACCATCACGGGCAACACAGCACTTCTCAGAGGTTCCAGGGGATCTTACCGTGC 368  
Qy 115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134  
Db 369 TTTCGACAGCATAAGTGGGCGCCCATGTCCTCCATGAGATCCGGCTC-----416  
Qy 135 LeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValVal-----150  
Db 417 ATGGCCGAGGGTGGCCCGCCCAAGTGGCAAGAGAGAGTGAAGCCCGTGGAGTGGAGGAA 476  
Qy 151 GlyGluGlnPheThrLeuGluCysGlyProProThrGlyHisProGluProThrValSer 170  
Db 477 GGGGAGTCAGTGGTTCGCTTGTCAACCTTCC-----CCAAAGTGAGAGCCCTCTCCGGATC 533  
Qy 171 TrpTyrAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly---189  
Db 534 TACTGGATGAACAGCAGATCTTCACATCAGCAGGAGCGGGTGCACGATGGGCCAG 593  
Qy 190 ---GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*Thr---TyrMetCys 207  
Db 594 AACGGCAACCTCTACTTTGCCAATGTGCTCACCTCCGACCAACCACTCAGACTACATCTGC 653  
Qy 208 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 227  
Db 654 -----CAGCCCATCTTCCAGGCACAGACCATCATTCAGAAAG 692  
Qy 228 ProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAsnVal 247  
Db 693 -----GAACCATTTGACCTC-----CGGGTCAAGGCCCAACCAAC---725  
Qy 248 ThrLeuLeuAsnProAspPro-AlaGluGlyProLysProArgProAlaVal-----264  
Db 726 AGCATGATTGACGAGGAGCGGCTGTCTTCCCACTCCCACTCCAGCAGCCACCTGGTG 785



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,886  
FILING DATE:  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 2626  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 4608 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..4342

US-09-041-886-24

Alignment Scores:  
Pred. No.: 1.2e-07 Length: 4608  
Score: 206.00 Matches: 68  
Percent Similarity: 42.80% Conservativeness: 36  
Best Local Similarity: 27.98% Mismatches: 97  
Query Match: 12.81% Indels: 42  
DB: 3 Gaps: 11

US-10-047-021-86 (1-303) x US-09-041-886-24 (1-4608)

QY 51 MetSerCysArgAlaSerGlyGlnProProThrIleAgtTrpLeuLeuAsnGlyGln 70  
DB 475 CTCAGTGTGAAGTATGGGAGCCCATCCACACATCCACTGCAGAGAGACCAACA 534  
QY 71 ProLeuSerMetValProProAspProHis---HisLeuLeuProAspGlyThrLeuLeu 89  
DB 535 GACCTGACTCCAAATCCAGGTGACTCCGAGTGGTGTCTTCCCTCTGGAGCATTTGCAG 594  
QY 90 Leu-----LeuGlnProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThr 107  
DB 595 ATCAGCCGACTCCAAACCG-----GGG 615  
QY 108 AspLeuGlyValThrCysGluAlaSerAenArgLeuGlyThrAlaValSerArg--- 126  
DB 616 GACATTGGAATTTACCGATGCTCAGATCCAGACTGCATAGACAGCTGTATT 666  
QY 127 GlyAlaArgLeuSerValAlaValLeuArgGluAsp-----Phe 139  
DB 667 GGAATATGAAGCAGAGAGTCAAGATTTATCAGATCCAGGACTGCATAGACAGCTGTATT 726  
QY 140 GlnIleGlnProArgAspMetValAlaValGlyGluGlnPheThrLeuGluCysGly 159  
DB 727 CTGCAAGACCACCAATGTAGTAGCCCATGAAGGAAAAGATGCTGTCTCGAATTTGT 786  
QY 160 ProProTTPGlyHisProGluProThrValSerTTPTrpLysAspGlyLysProLeuAla 179  
DB 787 GTTTCT---GGTATCTCTCCCAAGTTTACCTGGTTACGAGCGGAGGAGTCAATCAA 843  
QY 180 LeuGlnProGlyArgHisThrValSerGlyGlySer---LeuLeuMetAlaArgAlaGlu 198  
DB 844 CTCAGGTCTAAAGATATTCTTTATTTGGTGGAGCAACTTGTCTTCTCAATGTGACA 903  
QY 199 LysSerAspGlu\*\*\*ThrTyrMetCysValAlaThrAenSerAlaGlyHisArgGluSer 218  
DB 904 GATGATGACAGTGGAGTACCTGTGTGTGCACATATATAAATAGAGATATTAGTGCC 963  
QY 219 ArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeu 238

Db 964 TCTGCAGAGCTCACAGTCTTGGTTCGCGCATGTTTAAATCATCTCTCCAACTGTAT 1023  
QY 239 Ala-----ValArgIleGlnLeuGluAenValThrLeuLeuAenProAspProAla 255  
DB 1024 GCCTATGAACGATGATATTGAGTTTGAATGTACAGTC-----1062  
QY 256 GluGlyProLysProArgProAlaValTrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*Arg 275  
DB 1063 ---TCTGGAAGCCTGTGCCACCTGTG-----AATTGGATGAAGAATGGAGATGGTGC 1113  
QY 276 LeuProAen 278  
DB 1114 ATTCCTAGT 1122

RESULT 11

PCT-US94-05277-1

Sequence 1, Application PC/TUS9405277

GENERAL INFORMATION:

APPLICANT: Bruskin, Arthur

APPLICANT: Jarosz, David E.

APPLICANT: Johnson, Karen

APPLICANT: Kinzler, Kenneth W.

APPLICANT: Vogelstein, Bert

APPLICANT: Zabrecky, James R.

TITLE OF INVENTION: Antibodies Specific for DCC Gene Product

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie & Beckett

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05277

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A. 32,141

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.42709

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202.508.9100

TELEFAX: 202.508.9299

TELEX: 197430 BMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4608 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Homo sapiens

POSITION IN GENOME: 18q21

CHROMOSOME/SEGMENT: 18q21

FEATURE:

NAME/KEY: CDS

LOCATION: 1..4342

PCT-US94-05277-1

Alignment Scores:

Pred. No.: 1.2e-07 Length: 4608

Score: 206.00 Matches: 68

Percent Similarity: 42.80% Conservativeness: 36

## RESULT 9

US-08-506-296B-13  
; Sequence 13, Application US/08506296B  
; Patent No. 6313265  
; GENERAL INFORMATION:  
; APPLICANT: Phillips, Greg  
; APPLICANT: Cunningham, Bruce A.  
; APPLICANT: Crossin, Kathryn L.  
; TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES  
; TITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: The Scripps Research Institute  
; STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: U.S.  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/506,296B  
; FILING DATE: 24-JUL-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSI 488.0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3888 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 12...3773  
US-08-506-296B-13

Alignment Scores:  
Pred. No.: 7,96e-08 Length: 3888  
Score: 207.00 Matches: 87  
Percent Similarity: 37.50% Conservative: 36  
Best Local Similarity: 26.52% Mismatches: 107  
Query Match: 12.87% Indels: 98  
DB: 4 Gaps: 17

US-10-047-021-86 (1-303) x US-08-506-296B-13 (1-3888)

Qy 26 MetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGlnGly 45  
Db 120 ATCCGGAACAGCTCTCCACGGCGCTGTGTCTTCCACAGATGACATC----- 170  
Qy 46 ProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThriLeArgTrp 65  
Db 171 -----AGCCTCAAGTGTAGCCAGTGGCAAGCCGAGTGCAGTTCGCTGG 218  
Qy 66 LeuLeuAenGlyGlnProLeuSerMetValProProAspProHisLeuLeuProAsp 85  
Db 219 ACGAGGATGTGTC-----CATTCAACCCAG 248  
Qy 86 GlyThrLeu-----LeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103

Db 249 GAAGAGCTGGGTGTGACCGGTGTACAGTCGCC-----CACTCTGGCTCC 293  
Qy 104 AlaLeuSerThrAsp-----LeuGlyValTyThrCys 114  
Db 294 TTCACCATCAGGGCAACAACAGCAACTTGTCTCAGAGTTTCCAGGGCATCTACCGTGC 353  
Qy 115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134  
Db 354 TTTGCCAGCAATAAGCTGGGCACCGCCATGTCTCCATGAGATCCGGCTC----- 401  
Qy 135 LeuArgGluAspPheGlnIleGlnProArgAspMetValAlaVal----- 150  
Db 402 ATGCCGAGGTGCCCAAGTGGCCAAAGAGACAGAGTGAAGCCCGTGGAGTGGAGGAA 461  
Qy 151 GlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSer 170  
Db 462 GGGAGTCAGTGTCTTGTTCCTTGAACCTCC-----CCAAGTGAGAGCCCTCTCGGATC 518  
Qy 171 TrpTrpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGly--- 189  
Db 519 TACTGGATGAACAGCAAGATCTTGCACATCAAGCAGCAGCGGTGACGATGGCCAG 578  
Qy 190 ---GlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*Thr---TyrMetCys 207  
Db 579 AACGGCAACCTCTACTTTGGCAATGTCTCACTCCGACCAACCACTCAGACTACATCTGC 638  
Qy 208 ValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGlu 227  
Db 639 -----CAGCCCACTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 677  
Qy 228 ProGlnAspTyrThrGluProValGluLeuAlaValArgIleGlnLeuGluAsnVal 247  
Db 678 -----GAACCATTTGACCTC-----CGGGTCAAGGCCCAACCAAC--- 710  
Qy 248 ThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAlaVal-----Tr 265  
Db 711 AGCATGATTGACAGGAAGCGCGCTGTCTTCTCCCACTCCAGCAGCAGCAGCAGCAGCAGCAG 770  
Qy 265 p-Leu\*\*\*TrpLysValSerGlyPro\*\*\*----- 274  
Db 771 GCCTTGAGGGGAGCGCATTTGCTCGAGTGCATCGCGAGGGCTTTCCACGCCCAACC 830  
Qy 275 -----ArgLeuProAsnLeuThrArgProCysSerGlyPro----- 286  
Db 831 ATCAATGGTGGCGCCCGCAGTGGCCCATGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 890  
Qy 287 -----ArgLeuProArgGluA 292  
Db 891 AACAAAGACCTGCAGCTGCTGAAGTGGCGGAGGAGTGTATGGCGAGTACCGCTGCTG 950  
Qy 292 laArgGluLeuArgGlyGln 298  
Db 951 GCCGAGAAGTCACTGGGCAG 970  
RESULT 10  
US-09-041-886-24  
; Sequence 24, Application US/09041886  
; Patent No. 6235872  
; GENERAL INFORMATION:  
; APPLICANT: Breiden, Dale E.  
; APPLICANT: Rabizadeh, Sharro  
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence  
; TITLE OF INVENTION: Polypeptides and Methods of Use  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk





STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/158,657  
FILING DATE: US/09/158,657

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/800,825  
FILING DATE: 14-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-158-657-6

Alignment Scores:  
Pred. No.: 8,31e-11 Length: 6000  
Score: 246.00 Matches: 94  
Percent Similarity: 44.13% Conservative: 45  
Best Local Similarity: 29.84% Mismatches: 101  
Query Match: 15.30% Indels: 77  
DB: 3 Gaps: 17

US-10-047-021-86 (1-303) x US-09-158-657-6 (1-6000)

Qy 2 GlySerGlyGlyAspSerLeuLeuGlyArgGlySerLeuProLeuLeuLeuLeu 21  
Db 38 GGCCCTGGCATGTGTCGTGGTGGTCCATCGGC-----CTCTTGTTGTCCTG 88

Qy 22 IleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGln 41  
Db 89 CTCGTTGGAGGCTGTGACACAGAAGGCCCGCCCGGTTTATCAAGAACCCCAAGACCAG 148

Qy 42 LeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProPro 61  
Db 149 ATCGCGCTGCGGGCGTGTGCGCTCTTCGTGTGTGACGCCACCGGTGACCCCAAGCCA 208

Qy 62 ThrIleArgTrp-----LeuLeuAnGlyGlnProLeuSerMetValPro 76  
Db 209 CGAGTAGCTGGAACAAGAAAGGCAAGAGGTCAACTCTCACGCGTTTTGAGACGATTGAG 268

Qy 77 ProAspProHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArg 96  
Db 269 TTTGATGAG-----AGTCGAGGCGGAGTGTGAGATCCAGCCG----- 307

Qy 97 GlyHisAlaHisAspGlyGlnAlaLeuSerThr-----AspLeuGlyValTyThrCys 114  
Db 308 -----CTGAGGACACCGCGGGATGAACGTTGACGAGTGT 343

Qy 115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValalaVal 134  
Db 344 GTGGCCCAACTCGGTTGGG---GAGATCACAGTCCATGCCCAGCTTACT-----GTC 394

Qy 135 LeuArgGluAsp-----PheGlnIleGlnProArgAspMet 146  
Db 395 CTCGAGAGGACCAACGCTGCGCTTCTGCTTCCCCAACAATCGACATGGGCCCAAGTTGAAG 454







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Qy 32 ProGlnIleLeuValHisProGlnAaspGlnLeuPheGlnGlyProGlyProAlaArgMet 51
Db 790 CCGCGATCACTCCGAGCCCGGAGCGAGATGTGACCTCGGGAAACACCGTGTACTTC 849
Qy 52 SerCysArgAlaSerGlyGlnProProProProThrIleArgTrpLeuLeuAasnGlyClnPro 71
Db 850 ACCTGCAGAGCGGAGGCAACCCCAAGCTCGATCATCTGCTCGGAAACAATAATGAG 909
Qy 72 LeuSerMetValProProAaspProHisIleLeuLeuProAaspGlyThrLeuLeuLeuLeu 91
Db 910 CTGACATGAGACAGATCCCGCTAACTTCCTGGAGATGGAGACCTGATGATC--- 966
Qy 92 GlnProProAlaArgGlyHisAlaHisAaspGlyGlnAlaLeuSerThrAaspLeuGlyVal 111
Db 967 -----CAGAACACACAGGACAGACAGGCGGTATC 996
Qy 112 TyrThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSer 131
Db 997 TACCAGTGCATGGCAAGAACGCTGCCCGGAGGTGAAGACGCAAGAGGTGACCCCTCAGG 1056
Qy 132 Val-----AlaValLeuArgGluAaspPheGlnIleGlnProArgAaspMetValAlaVal 149
Db 1057 TACTTCGGGTCTCCAGCTCGACCCACTTTTGTATCCAGCCACAGATACAGAGGTGCTG 1116
Qy 150 ValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrVal 169
Db 1117 GTTGGGAGAGCGTCACGCTGGAGTGCAGGCCACA---GGCCACCCCGCGCGGATC 1173
Qy 170 SerTrpTrpLys---AsgGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSer 188
Db 1174 TCCTGCAGAGAGGTGACCGCACACCTTTCAGTGTGACCGCGGTGGAACATCACGCGCT 1233
Qy 189 GlyGlySerLeuLeuMetAlaArgAlaGluLysSerAaspGlu**ThrTyrMetCysVal 208
Db 1234 TCTGGCGGGCTTTACAGAACCTCGTACAGGGGGACGCGGAGATATCGGTCTCT 1293
Qy 209 AlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluPro 228
Db 1294 GCGACCAACAACATTGACAGCGTCCATGCCCGCTTTCATCATCGTCCAGGCTCTTCT 1353
Qy 229 GlnAaspTyrThrGluProValGluLeuLeuAlaValArgIleGlnLeuGluAasnValThr 248
Db 1354 CAGTTCACTGTGACGCGCTCAGGAC-----AGAGTCTGTTATTGAGGGGCCAGACC 1401
Qy 249 Leu-Leu-----AasnProAaspProAlaGln 256
Db 1402 GTGGATTTCCAGTGTGAAGCCAGGCGCAACCGCGCGCTTCATCGCTCGACCAAGGGA 1461
Qy 256 uGly-Pro-----LysProArgProAlaVal----- 264
Db 1462 GGGAGCCAGCTTCGCTGGAGCGCGGACCTGCTGTCATCGGGAACACTTAGAATC 1521
Qy 265 ---TrpLeu**TrpLysValSerGlyPro**ArgLeuProAasnLeuThrArgProCys 284
Db 1522 TCTGTGTGTGCTCCACGACGAGGCGCAGTACGAATGCCAGGC-----TGTC 1569
Qy 284 erGlyProArgLeuProArgGluAlaArgGluLeuArgGly----- 297
Db 1570 AACATCATCGGCTCCCA-----GAAGTCTGTGGCCCACTGACTGTGCGAGCCC 1617
Qy 298 -----GlnArgArgAasnThrGly 303
Db 1618 AGAGTCACCCAGTGTGTCAGCATTTCCAGCGACACACAGTGA 1664
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## RESULT 2

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US-09-016-434-1132
; Sequence 1132, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
```

```
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1132:
SEQUENCE CHARACTERISTICS:
LENGTH: 4078 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1407624
US-09-016-434-1132
Alignment Scores:
Pred. No.: 5,09e-11 Length: 4078
Score: 246.00 Matches: 94
Percent Similarity: 44.13% Conservative: 45
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Query Match: 15.30% Indels: 77
DB: 4 Gaps: 17
US-10-047-021-86 (1-303) x US-09-016-434-1132 (1-4078)
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Qy 22 IleMetGlyGlyMetAlaGlnAaspSerProGlnIleLeuValHisProGlnAaspGln 41
Db 89 CTCGTGGAGCTGTGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
Qy 42 LeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 61
Db 149 ATCGGCGGTGCGGGCGGTGCTCTTCTGTGTGTCAGGCCACGCGGTGACCCCAAGCCA 208
Qy 62 ThrIleArgTrp-----LeuLeuAasnGlyGlnProLeuSerMetValPro 76
Db 209 CGAGTGACCTGGAAACAAGAGGGCAAGAGTCACTCTCAGCGCTTTGACAGCATTCAG 268
Qy 77 ProAaspProHisHisLeuLeuProAaspGlyThrLeuLeuLeuLeuGlnProProAlaArg 96
Db 269 TTTGATGAG-----AGTGCAGGGCGAGTGTGCTGAGGATCCAGCCG----- 307
Qy 97 GlyHisAlaHisAaspGlyGlnAlaLeuSerThr-----AaspLeuGlyValTyrThrCys 114
Db 308 -----CTGAGGACACCGCGGGATGAAACACGTGTACGAGTGT 343
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2004, 12:35:25 ; Search time 66.4611 Seconds  
(without alignments)  
2012.290 Million cell updates/sec

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Perfect score: 1608  
Sequence: 1 MGSGDLSLGGKSGSLPLLL.....SGPRLPREARELQRRNTG 303

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	276.5	17.2	6814	US-09-484-970B-66	Sequence 66, Appl
2	246	15.3	4078	US-09-016-434-1132	Sequence 1132, Ap
3	246	15.3	6000	US-08-348-006B-6	Sequence 6, Appl
4	246	15.3	6000	US-08-800-825A-6	Sequence 6, Appl
5	246	15.3	6000	US-09-158-657-6	Sequence 6, Appl
6	246	15.3	6000	PCT-US94-10166-6	Sequence 6, Appl
7	237.5	14.8	5890	US-08-447-464-2	Sequence 2, Appl
8	237.5	14.8	5890	US-08-716-679-2	Sequence 2, Appl
9	207	12.9	3888	US-08-506-296B-13	Sequence 13, Appl
10	206	12.8	4608	US-09-041-886-24	Sequence 24, Appl
11	206	12.8	4608	PCT-US94-05277-1	Sequence 1, Appl
12	201.5	12.5	3398	PCT-US95-08493-12	Sequence 12, Appl

13	199	12.4	1042	2	US-08-427-497E-6	Sequence 6, Appl
14	199	12.4	1426	4	US-09-638-649-2	Sequence 2, Appl
15	199	12.4	3774	2	US-08-341-843B-1	Sequence 1, Appl
16	199	12.4	3774	2	US-08-427-497E-1	Sequence 1, Appl
17	199	12.4	3774	2	US-08-427-497E-2	Sequence 2, Appl
18	196.5	12.2	4078	4	US-09-016-434-1120	Sequence 1120, Ap
19	195	12.1	3991	4	US-08-506-296B-3	Sequence 3, Appl
20	194.5	12.1	3943	4	US-08-506-296B-27	Sequence 27, Appl
21	192	11.9	3189	2	US-08-427-497E-3	Sequence 3, Appl
22	191	11.9	3783	4	US-08-506-296B-20	Sequence 20, Appl
23	189	11.8	4843	3	US-08-986-485-1	Sequence 1, Appl
24	185.5	11.5	1391	4	US-09-638-649-4	Sequence 4, Appl
25	182.5	11.3	5824	4	US-09-620-312D-72	Sequence 72, Appl
26	177.5	11.0	3551	4	US-09-620-312D-760	Sequence 760, App
27	175.5	10.9	1493	2	US-08-752-307B-6	Sequence 6, Appl
28	175.5	10.9	1493	4	US-09-707-802-6	Sequence 6, Appl
29	175.5	10.9	1493	4	US-09-991-326-6	Sequence 6, Appl
30	172	10.7	957	2	US-08-633-148-3	Sequence 3, Appl
31	172	10.7	1023	2	US-08-633-148-1	Sequence 1, Appl
32	170.5	10.6	3360	1	US-08-408-093-5	Sequence 5, Appl
33	170.5	10.6	3360	1	US-08-408-420A-5	Sequence 5, Appl
34	170.5	10.6	3360	1	US-08-714-901-5	Sequence 5, Appl
35	170.5	10.6	3360	3	US-08-040-741-5	Sequence 5, Appl
36	170.5	10.6	3453	4	US-09-877-730-7	Sequence 7, Appl
37	169.5	10.5	1143	4	US-09-877-730-3	Sequence 3, Appl
38	169.5	10.5	2715	4	US-09-877-730-5	Sequence 5, Appl
39	169.5	10.5	2958	4	US-09-877-730-9	Sequence 9, Appl
40	169.5	10.5	3210	4	US-09-877-730-1	Sequence 1, Appl
41	167.5	10.4	3874	4	US-09-877-730-31	Sequence 31, Appl
42	167	10.4	3014	2	US-08-808-982-1	Sequence 1, Appl
43	167	10.4	3014	3	US-09-306-902A-1	Sequence 1, Appl
44	166.5	10.4	1967	3	US-09-383-586-22	Sequence 22, Appl
45	165.5	10.3	2610	1	US-08-374-834-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-09-484-970B-66  
; Sequence 66, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmath, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 66  
; LENGTH: 6814  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 199882.3  
; NAME/KEY: unsure  
; LOCATION: 1838, 5528  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-484-970B-66  
  
Alignment Scores:  
Pred. No.: 2.96e-13 Length: 6814  
Score: 276.50 Matches: 93  
Percent Similarity: 38.80% Conservative: 30  
Best Local Similarity: 29.34% Mismatches: 125  
Query Match: 17.20% Indels: 69  
DB: 4 Gaps: 11  
  
US-10-047-021-86 (1-303) x US-09-484-970B-66 (1-6814)

PN W09925833-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 13-NOV-1998; 98WO-US24327.  
XX  
PR 14-NOV-1997; 97US-0065543.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
PI Goodman C, Kid T, Mitchell KJ, Russell C, Tear G;  
XX  
DR WPI; 1999-338008/28.  
DR P-PSDB; MAY13566.  
XX  
PT Modulation of Robo-Comm polypeptide interactions  
XX  
PS Disclosure; Page 42-44; 56pp; English.  
XX  
XX The invention relates to a method for modulating the amount of Comm  
CC (commisoreless) polypeptide in contact with a cell expressing active  
CC Robo (roundabout) on its surface. The method comprises modulating the  
CC effective amount of Comm polypeptide in contact with the cell, where the  
CC amount of expressed active Robo is specifically modulated inversely with  
CC the modulation of the effective amount of Comm in contact with the cell.  
CC The method is used to modulate the amount of active Robo expressed on a  
CC cell. The method can be used to screen for agents that modulate Robo:Comm  
CC interactions. This is particularly useful for modulating nerve cell  
CC function.  
XX  
SQ Sequence 4956 BP; 1480 A; 1230 C; 1186 G; 1060 T; 0 other;

Alignment Scores:  
Pred. No.: 3,09e-19 Length: 4956  
Score: 446.50 Matches: 98  
Percent Similarity: 54.36% Conservative: 33  
Best Local Similarity: 40.66% Mismatches: 95  
Query Match: 27.77% Indels: 16  
DB: 20 Gaps: 3

US-10-047-021-86 (1-303) x AAX55770 (1-4956)

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Db 122 GGAGCCCAATCCCACTCTGATACGATGACAAATTCGCTG-GGCTATACAGGCTCCCGT 180  
QY 28 -----GlnAspSerProGlnLeuValHisProGlnAspGlnLeuPheGln 44  
Db 181 CTTCGTCAGGAAGATTTTCCACCTCGCATTTGTAACACCCCTTCAGACCTGATTGTCTCA 240  
QY 45 GlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArg 64  
Db 241 AAAGAGAACCTTGCACTTGAACCTGCAAGCTGAGGCCGCCCCACACCCACTATTGAA 300  
QY 65 TrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHis----- 81  
Db 301 TGGTACAAAGGGGAGAGAGTGGAGACAGACAGAAAGATGACCTTCGCTCACCCGAATG 360  
QY 82 LeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAsp 101  
Db 361 TTGCTGCCGAGTGGATCTTTATTTTCTTACGT-----ATAGTACAT 402  
QY 102 GlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGly 121  
Db 403 GGACGGAAGAGTAGACCTGATGAAGAGTCTATGTCTGTGTAGCAAGGAATTACCTTGA 462  
QY 122 ThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIle 141  
Db 463 GAGGCTGTGAGCCCAATGCATCGCTGGAAGTAGCCATACITCGGGATGACTTCAGACAA 522  
QY 142 GlnProArgAspMetValAlaValAlaValGlyGlnGlnPheThrLeuGluCysGlyProPro 161  
Db 523 AACCCCTCGGATGTCATGTTGTCAGTAGGAGAGCCCTGCAGTAATGGAATGCCAACCTCCA 582

QY 162 TrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGln 181  
Db 583 CGAGGCCATCCTGAGCCACCACCATTTTCATGAAGAAAGATGGCTCTCCACTGGATGATAAA 642  
QY 182 ProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAsp 201  
Db 643 GATGAAGAATAACTATACGAGGAGGAAGCTCATGATCACTTTACACCCCGTAAAGTGAC 702  
QY 202 Glu\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAla 221  
Db 703 GCTGGCAATATGTTGTGTGTGTACCAATATGTTGGGAACGTGAGAGTGAAGTAGCC 762  
QY 222 ArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArg 241  
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QY 242 Ile 242'  
Db 823 GTG 825

Search completed: January 31, 2004, 12:48:08  
Job time : 254.772 secs

Db 574 GTGGCTCAGCTGGAAGTCAAGTGGCCCTGCTCGGCTGCCAATCTTACAGCGCTTGT 633  
QY 284 exGlyProArgLeuProArgGluAlaArgGluLeuArgGlnArg 299  
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## RESULT 14

AAV69278  
ID AAV69278 standard; cDNA; 4291 BP.

XX AAV69278;

DT 01-MAR-1999 (first entry)

XX Human T85 cDNA.

XX T85; FMHB-6D4; FMHV-SD4; human; neurological disorder; therapy;  
KW diagnosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 958..3219

FT /\*tag= a

FT sig\_peptide 958..1017

FT /\*tag= b

FT mat\_peptide 1018..3216

FT /\*tag= b

XX WO9848051-A2.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-US07714.

XX 10-OCT-1997; 97US-0062017.

XX 18-APR-1997; 97US-0044746.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Holtzman D, McCarthy SA;

XX WPI; 1999-024021/02.

XX P-PSDB; AA83927.

XX New isolated human FTHMA-070 and T85 proteins - used to develop  
PT products for the diagnosis and therapy of disorders involving  
PT cellular processes, e.g. neuronal development.

XX Claim 24; Fig 3; 127pp; English.

XX This claimed cDNA sequence, the coding region of which is also  
CC claimed, codes for novel human T85 (see AA83927), also referred to  
CC FMHB-6D4 and FMHB-SD4. The cDNA was identified in a human foetal  
CC brain cDNA library using a screen designed to identify genes  
CC encoding proteins having a functional signal sequence. T85 nucleic  
CC acids and polypeptides of the invention are useful as modulating  
CC agents in regulating a variety of cellular processes. They can be  
CC used for identifying compounds which bind to or modulate the  
CC activity of the polypeptides (claimed). They can also be used in  
CC screening assays, detection assays (e.g. chromosomal mapping,  
CC tissue typing, forensic biology), predictive medicine (e.g.  
CC diagnostic assays, prognostic assays, monitoring clinical trials,  
CC and pharmacogenomics), and methods of treatment (e.g. therapeutic  
CC and prophylactic) e.g. for neurological disorders.

XX Sequence 4291 BP; 1154 A; 1011 C; 1045 G; 1081 T; 0 other;

## Alignment Scores:

Pred. No.: 1.03e-19 Length: 4291  
Score: 453.00 Matches: 98  
Percent Similarity: 54.51% Conservative: 35

Best Local Similarity: 40.16% Mismatches: 98  
Query Match: 28.17% Indels: 13  
DB: 20 Gaps: 3

US-10-047-021-86 (1-303) x AAV69278 (1-4291)

QY 6 AspSerLeuLeuGlyArgGlySerLeuProLeuLeu-LeuLeuLeuIleMetGly 25  
Db 954 GACAATGATTCGGGAGCCGCTCACTTTACTCTGTTGGATTATATCTCTCTGTTGAG 1013

QY 25 Y-----MetalGlnAspSerProGlnIleLeuValHisProGlnAspGlnLe 42  
Db 1014 CTCCTCGTTCGTCAGGAAGATTTTCCACCTCGCATGTTGCAACACCTTTCAGACCTGAT 1073

QY 42 uPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProTh 62  
Db 1074 TGTCTCAAAAGGAGAACCTGCAACTTGAACCTGAAAGCTGAAGCCGCCCCACCCAC 1133

QY 62 rIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHis-- 81  
Db 1134 TATTGAATGGTACAAAGGGGAGAGAGAGTGGAGACAGACAAAGATGACCTCGCTCACA 1193

QY 82 -----LeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAl 99  
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QY 99 aHisAspGlyGlnAlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnAr 119  
Db 1236 AGTACATGGACGGAAAGTAGACCTGATGAAGGAGTCTATGCTGTGTAGCAAGAAATA 1295

QY 119 gLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPh 139  
Db 1296 CCTTGGAGAGGCTGTGAGCCACAATGCATCGCTGGAAGTAGCCATCTTCCGGATGACTT 1355

QY 139 eGlnIleGlnProArgAspMetValAlaValAlaValGlyGlnGlnPheThrLeuGluCysGl 159  
Db 1356 CAGACAAAACCCCTTCGGATGTGCATGGTTGCAGTAGGAGAGCCCTGCAGTAATGAATGCCA 1415

QY 159 yProProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyIysProLeuAl 179  
Db 1416 ACCTCCACGAGGCCATCTGTAGCCACCATTTCAATGAAGAAGATGGCTCTCCACTCGA 1475

QY 179 aLeuGlnProGlyArgHisThrValSerGlyIysSerLeuLeuMetAlaArgAlaGluLy 199  
Db 1476 TGATAAAGATGAAGAATAACTATACGAGGAGGAAGCTCATGATCATCTTACACCCGTAA 1535

QY 199 sSerAspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerAr 219  
Db 1536 AAGTCACGCTGGCAAAATATGTTGTGTTGTTACCAATATGTTGGGGAACCTGAGAGTGA 1595

QY 219 gAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAl 239  
Db 1596 AGTAGCCGAGCTGACTGTCTTAGAGAGACCAATCAATTTGTGAAGAGACCCAGTAACCTGGC 1655

QY 239 aValArgIle 242

Db 1656 AGTAACGTGTG 1665

## RESULT 15

AAAX55770

ID AAAX55770 standard; cDNA; 4956 BP.

XX AAAX55770;

XX 30-JUL-1999 (first entry)

XX Human Robo 1 polypeptide encoding cDNA.

XX Comm polypeptide; Robo polypeptide; commissureless; roundabout;  
KW modulation; nerve cell function; ds.  
XX Homo sapiens.

Qy 279 uThArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnAr 299  
 Db 876 TACACAGCTCTGTTTCAGGACTCAGAGGTCTCCCGAGGACCAAGGATCTCCATGACAGAG 935  
 Qy 299 g 239  
 Db 936 g 936

RESULT 13  
 AAS01694  
 ID AAS01694 standard; cDNA; 3042 BP.  
 XX AC AAS01694;  
 XX 18-JUL-2001 (first entry)  
 XX DE Human TANGO 330 form 1 cDNA sequence.  
 XX Human; TANGO 315; clone jthAa060g22; TANGO 330; TANGO 437; TANGO 480;  
 KW cellular process regulator; gene therapy; adrenal gland; cancer; ss;  
 KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;  
 KW cell proliferative disorder; neurological disorder; Alzheimer's disease.  
 XX OS Homo sapiens.  
 XX FH Key  
 XX CDS  
 XX Location/Qualifiers  
 XX 2..2806  
 XX /tag= a  
 XX /partial  
 XX /product= "TANGO 330 form 1 protein"  
 XX /note= "The ORF is specifically claimed. This sequence  
 variation replace (4,C)  
 FT /tag= b  
 FT variation replace (5,T)  
 FT /tag= c  
 FT variation replace (9,T)  
 FT /tag= d  
 FT variation replace (159,A)  
 FT /tag= e  
 FT  
 FN WO200123523-A2.  
 XX  
 XX 05-APR-2001.  
 XX 02-OCT-2000; 2000WO-US27202.  
 XX 30-SEP-1999; 99US-0409634.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Kirst S, Wrighton N, Fraser CC;  
 XX WPI; 2001-235372/24.  
 XX P-PSDB; AAU00500.  
 XX Isolated secreted proteins and their encoding nucleic acids are used  
 XX for diagnosis and treatment of e.g. bacterial and viral infections,  
 XX autoimmune diseases and inflammatory disorders -  
 XX Claim 2; Fig 13; 261pp; English.  
 XX The present sequence encoding for human TANGO 330 form 1 is  
 XX isolated from cDNA clone jthAa060g22 from a human adrenal gland  
 XX cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins  
 XX which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)  
 XX and TANGO 480 (AAU00503). The nucleic acids encoding these proteins  
 XX are useful as modulating agents in regulating a variety of cellular  
 XX processes and can be used to express the proteins in a host cell in  
 XX gene therapy applications. Antisense nucleic acid molecules and  
 XX expression vectors containing the TANGO nucleic acids are also described.  
 XX Diagnostic assays can be used to detect genetic alterations in the TANGO  
 XX nucleic acids and to identify compounds that bind to or modulate activity

CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to  
 CC monitor protein levels in tissue as a clinical testing procedure.  
 CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids  
 CC and proteins may be used to diagnose, treat and monitor disorders of the  
 CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They  
 CC can also be used to treat cell proliferative disorders (e.g. cancer),  
 CC and neurological disorders e.g. Alzheimer's disease.  
 XX  
 SQ Sequence 3042 BP; 607 A; 1008 C; 859 G; 568 T; 0 other;

Alignment Scores:  
 Pred. No.: 3.27e-61 Length: 3042  
 Score: 1104.50 Matches: 222  
 Percent Similarity: 74.75% Conservative: 0  
 Best Local Similarity: 74.75% Mismatches: 4  
 Query Match: 68.69% Indels: 71  
 DB: 22 Gaps: 1

US-10-047-021-86 (1-303) x AAS01694 (1-3042)

Qy 5 GlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuMetGly 24  
 Db 1 GGAGACAGCCCTCTGGGGGCGAGGGTTCCTGCTCTGCTCTGCTCTGCTCTATC----- 54  
 Qy 25 GlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPheGln 44  
 Db 54 ----- 54  
 Qy 45 GlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIleArg 64  
 Db 54 ----- 54  
 Qy 65 TrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeuPro 84  
 Db 54 ----- 54  
 Qy 85 AspGlyThrLeuLeuLeuLeuGln-ProProAlaArgGlyHisAlaHisAspGlyGlnAl 104  
 Db 55 -----ATGGCCCTCTGCGGGGACATGTCCTGCGGAGAGATTCAGATCCAGCTCG 93  
 Qy 104 aLeuSerThrAspLeuGlyValThrCysGluAlaSerAsnArgLeuGlyThrAlaVa 124  
 Db 94 CCTGTCACAGACTCGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGCCACGGCAGT 153  
 Qy 124 lSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnProAr 144  
 Db 154 CAGCAGAGGGCGCTCGGTGTCTGTGCTGTCTCTCGGAGAGATTCAGATCCAGCTCG 213  
 Qy 144 gAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHi 164  
 Db 214 GGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCGCCCTGGGGCCA 273  
 Qy 164 sProGluProThrValSerTrpTrpIysAspGlyLysProLeuAlaLeuGlnProGlyAr 184  
 Db 274 CCCAGAGCCACAGTCTCATGTGTGGAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAG 333  
 Qy 184 gHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*Th 204  
 Db 334 GCACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGAGCAGAGAGAGTAGTACGAGGGGAC 393  
 Qy 204 rTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValse 224  
 Db 394 CTACATGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCGCGCGCGGGTTTC 453  
 Qy 224 rIleGlnGluProGlnAspTrpThrGluProValGluLeuLeuAlaValargIleGlnLe 244  
 Db 454 CATCCAGAGAGCCCGAGGACTACACGGAGCCTGTGGAGCTTCTGCTGTGCGAATTCAGCT 513  
 Qy 244 uGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProIlysProArgProAlaVa 264  
 Db 514 GGAAATGTGACACTGTGTAAACCCGGATCTCTGACAGGGGCCCCAGGCTAGACGGCGGT 573  
 Qy 264 lTrpLeu\*\*\*TrpIysValSerGlyPro\*\*\*-ArgLeuProAsnLeuThrArgProCysS 284



QY 201 AspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220  
Db 640 GACGAGGACCTACATGTGTGTGGC-ACCAACAGCGCAGGACACAGGAGAGCCGNGCA 698  
QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAla 239  
Db 699 CC-CGGGTTTNCATTACGAGGCCCCANGACTACACGGAACCTGTGGAACTTTTGGCT 754

## RESULT 12

ID ABK87138  
XX ABK87138 standard; cDNA; 3688 BP.

AC ABK87138;  
XX

DT 07-OCT-2002 (first entry)  
XX

DE cDNA mouse ECSM4 protein.  
XX

XX Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculature;  
KW imaging vascular endothelium; proliferative disease; cancer;  
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;  
KW endothelial damage; tumour neovasculature; cardiac disease;  
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;  
KW cardiant; gene; ss.  
XX

OS Mus sp.  
XX

XX Key Location/Qualifiers  
FH 6..3053  
CDS

FT /\*tag= a  
FT /note= "ECSM4 #1"  
FT 3393..3512

FT /\*tag= b  
FT /note= "ECSM4 #2"  
FT 3579..3683

FT /\*tag= c  
FT /note= "ECSM4 #3"  
FT

XX WO200236771-A2.  
XX

XX 10-MAY-2002.  
XX

XX 06-NOV-2001; 2001WO-GB04906.  
XX

XX 06-NOV-2000; 2000US-245566P.  
XX

XX 07-MAR-2001; 2001US-273662P.  
XX

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
XX

XX Bicknell R, Huminiecki L;  
XX

XX WPI; 2002-508120/54.  
XX

XX P-PSDB; AAU99420, AAU99421, AAU99422.  
XX

XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for  
PT imaging, diagnosing and treating a condition involving vascular  
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes  
XX

XX Disclosure; Fig 13; 248pp; English.  
XX

XX The present invention relates to endothelial cell-specific molecule 4  
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4  
CC proteins are useful for imaging vascular endothelium in the body of  
CC an individual, and for diagnosing and treating a proliferative  
CC disease or condition involving the vascular endothelium (preferably,  
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,  
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in  
CC the manufacture of diagnostic or prognostic agent for such conditions.  
CC The proteins are also useful for detecting endothelial damage or  
CC activation, detecting a tumour or tumour neovasculature, cardiac  
CC disease, or endometriosis by detecting the amount of ECSM4 present in  
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in  
CC gene therapy for treating a hypoxic condition such as cancer, cardiac

CC disease, endometriosis or atherosclerosis and in the manufacture of  
CC medicaments for treating the above disease. The sequences are useful  
CC for modulating angiogenesis in an individual. The present sequence  
XX encodes mouse ECSM4 protein.

SQ Sequence 3688 BP; 801 A; 1115 C; 1011 G; 761 T; 0 other;

## Alignment Scores:

Pred. No.: 9.94e-64 Length: 3688  
Score: 1145.50 Matches: 223  
Percent Similarity: 82.06% Conservative: 24  
Best Local Similarity: 71.09% Mismatches: 52  
Query Match: 74.24% Indels: 2  
DB: 24 Gaps: 1

US-10-047-021-86 (1-303) x ABK87138 (1-3688)

QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20

Db 36 ATGGGCTCTGGAGGAACGGGCTCTGGGGACGGAGTGGCTCTGCCTCTGCTGCTT 95

QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnasp 40

Db 96 TTCATCATGGGAGGTGAGGCTCTGGATTCTCCACCCAGATCCTAGTTTCACCCCGAGAC 155

QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60

Db 156 CAGTACTTTCAGGGCTCTGGCCAGCCAGATGAGTGCAGATCATTCGGGCAACCACT 215

QY 61 ProThrIleArgTyrLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80

Db 216 CCCACTATCCGCTGGCTGCTGAATGGGAGGCTCTGAGCATGGCCACCCAGACCTACAT 275

QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100

Db 276 TACCTTTTGGCGGATGGGACCTCTCTGTATCATCGGCCCTCTGTCCAGGGACGGCACAA 335

QY 101 AspGlyGln---AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArg 119

Db 336 GATGACCAAGAATCTCTCAGCAATCTTGGGTCTTACACATGTGAGCCAGCAACCGG 395

QY 120 LeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPhe 139

Db 396 CTGGGCACAGCAGTGAGCGGGTGTAGGCTGTCTGGCTGTCTCCAGAGGAGCTTC 455

QY 140 GlnIleGlnProArgAspMetValAlaValGlyGlnGlnPheThrLeuGluCysGly 159

Db 456 CAGATCCAACTCGGGACACAGTGGCGCTGTGGGAGAGAGCTTGGTCTTTGAGTGGT 515

QY 160 ProProTyrGlyHisProGluProThrValSerTyrTrpTyrAspGlyLysProLeuAla 179

Db 516 CTTCCCTGGGCTACCCAAACCTCTGGTCTCATGTGGTGGAAAGAGGAAACCTCTGGTC 575

QY 180 LeuGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLys 199

Db 576 CTCCAGCAGGAGGCGCAGATATCTGGGATTCCTGTGGTGTCAAGAGCAGAGAG 635

QY 200 SerAspGlu\*\*\*ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArg 219

Db 636 AATGACTCGGGGACCTATATGTGTATGCCACCAACAATGTGGGCAACGGGAGAGCGGA 695

QY 220 AlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAla 239

Db 696 GCAGCCAGGGTGTCTATCCAGGAATCCAGAGACCAAGGAACATCTAGAGCTTCTGGCT 755

QY 240 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259

Db 756 GTTCGCATTGAGCTGGAAAATGTGACCTCTGTAACCCCGAACCTGTAAAAGGTCCCAAG 815

QY 260 ProArgProAlaValTyrLeu\*\*\*TyrPlysValSerGlyPro\*\*\*ArgLeuProAsnLe 279

Db 816 CTTGGGCCCTCGGTGGCTCAGCTGGAAAGTGTAGCGGCCCTGTGTCACCTGTGAGTGCA 875

Db CGGACATGGTGGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGCCGCCCTGGGCG 590  
Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183  
Db 591 CACCAGAGCCACACAGTCTCATGTGGTGAAGATGGAAACCCCTGGCCCTCCAGCCCGGA 650  
Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\* 203  
Db 651 AGGCACACAGTGTCCGGGGGGTCCCTGCTGTGATGGCAGAGCAGAGAGTGTACGAGGG 710  
Qy 204 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223  
Db 711 ACCTACATGTGTGGCCACCAACAGCGACGACATAGCGAGCGCGCGCGGTT 770  
Qy 224 SerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValIleGln 243  
Db 771 TCCATCCAGGAGCCCCAGGACTACACGAGGCTGTGGAGCTTCTGGCTGTGCGAATTGAG 830  
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263  
Db 831 CTGGAARATGTGACACTCTGAACCCGGATCTCTGCAGAGGGCCCCAAGCCTAGACCGCG 890  
Qy 264 ValTrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*ArgLeuProLeuLeuThrArgProCys 283  
Db 891 GTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGTGTGGCCCTGGCCCAATCTTACAGCGCCTTG 950  
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
Db 951 TTCAGGACCCAGACTGTCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGG 999

## RESULT 11

AAH08234

ID AAH08234 standard; cDNA; 756 BP.

XX AC AAH08234;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA clone (5'-primer) SEQ ID NO:5069.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

XX PR 27-AUG-1999; 99JP-0300253.

XX PR 11-JAN-2000; 2000JP-0118776.

XX PR 02-MAY-2000; 2000JP-0183767.

XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX DR WPI; 2001-318749/34.

XX XX

XX PT Primer sets for synthesizing polynucleotides, particularly the 5602

XX PT full-length cDNAs defined in the specification, and for the detection

XX PT and/or diagnosis of the abnormality of the proteins encoded by the

XX PT full-length cDNAs -

XX PS Claim 1; SEQ ID 5069; 2537pp + CD ROM; English.

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

XX Sequence 756 BP; 147 A; 242 C; 236 G; 128 T; 3 other;

## Alignment Scores:

Pred. No.: 2,99e-67 Length: 756  
Score: 1190.00 Matches: 232  
Percent Similarity: 97.49% Conservative: 1  
Best Local Similarity: 97.07% Mismatches: 6  
Query Match: 74.00% Indels: 2  
DB: 22 Gaps: 0

US-10-047-021-86 (1-303) x AAH08234 (1-756)

Qy 1 MetGlySerGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20  
Db 40 ATGGGCTCTGGAGAGACAGCCTCTCTGGGGGAGGGTTCCTCGCTCTGCTCTCTG 99  
Qy 21 LeuIleMetGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40  
Db 100 CTATCATGGAGGATGGCTCAGGACTCCCGCCCGCCAGATCTTAGTCCACCCCGGAC 159  
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
Db 160 CAGCTGTTCCAGGCCCCTGGCCCTGCCAGGATGAGTGCACAGCCTCAGGCGCAGCACCT 219  
Qy 61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80  
Db 220 CCCACCATCCGCTGGTTGCTGAATGGGACGCCCTGAGCATGGTGGCCCGCCAGACCCAC 279  
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
Db 280 CACCTCTGCTGATGGGACCCCTCTCTGCTACAGCCCTCTGCCGGGACATGCCAC 339  
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTrpTrpCysGluAlaSerAsnArgLeu 120  
Db 340 GATGGCCAGGCCCTGTCCAGACCTGGGTGTCTACACATGTGAGGCGCAGCAACCGGCTT 399  
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140  
Db 400 GGACAGCGAGTACAGAGGCGCTCGGCTGTCTGTGGCTGTCTCCCGGAGGATTTCCAG 459  
Qy 141 IleGlnProArgAspMetValAlaValValGlyGlnPheThrLeuGluCysGlyPro 160  
Db 460 ATCCAGCCTCGAGACATGGTGGCTGTGGTGGGTGAGCAGTTTATCTCTGAATGTGGGCG 519  
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180  
Db 520 CCCTGGGCGCCACCAGAGGCCACAGTCTCATGTGGTGAAGATGAGAAACCCCTGGCCCTC 579  
Qy 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200  
Db 580 CAGCCCGGAGGACACAGTGTCCGGGGGGTCCCTGCTGTGATGGCAGAGCAGAGAGAGT 639

Db 241 CCTGATGGACCTTTCTGTCTACAGCCCTCGCCGGGAGCATGCCCCAGATGCCAG 300  
Qy 104 AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla 123  
Db 301 GCCCTGTCCACAGACTGGGTGTCTACACATGTGAGCCAGCACCGCTTGCGACGGCA 360  
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143  
Db 361 GTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCGGGAGGATTTCCAGATCCAGCT 420  
Qy 144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163  
Db 421 CGGACATGGTGGCTGTGGGTGAGCAGATTACTCTGGAATGTGGCGCGCTGGGGC 480  
Qy 164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183  
Db 481 CACCACAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCTCGCCCTCCAGCCCGGA 540  
Qy 184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\* 203  
Db 541 AGGCACACAGTCTCGGGGGGTCCCTGTCTGTATGGCAGAGCAGAGAGTGACGAGGG 600  
Qy 204 ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVal 223  
Db 601 ACCTACATGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCGGGT 660  
Qy 224 SerIleGlnProGlnAspTyrThrGluProValGluLeuAlaValArgIleGln 243  
Db 661 TCCATCCAGAGCCCGAGACTACAGGAGCCTGTGGAGCTTCTGGCTGTGGGAATTGAG 720  
Qy 244 LeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAla 263  
Db 721 CTGGAATGTGACACTGTGAACCGGATCTTCAGAGGGCCCCAGCCCTAGACCGGG 780  
Qy 264 ValTrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuThrArgProCy 283  
Db 781 GTGTGGCTCAGTGGGAAGTCACTGAGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 840  
Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
Db 841 TTCAGAGCCAGACTGCCCGGGAGGCCAGGAGTCCGTGGGCGAGAG 889  
RESULT 10  
AAS01695  
ID AAS01695 standard; cDNA; 3808 BP.  
XX AAS01695;  
AC AAS01695;  
DT 18-JUL-2001 (first entry)  
XX Human TANGO 330 form 2 cDNA sequence.  
DE Human TANGO 330 form 2 cDNA sequence.  
XX Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;  
KW cellular process regulator; gene therapy; astrocyte; cancer; ss;  
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;  
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
FH 9..1451  
FT CDS /tag= a  
FT /products= "TANGO 330 form 2 protein"  
FT /note= "The ORF is specifically claimed"  
FT sig\_peptide 9..68  
FT mat\_peptide 69..1448  
FT /tag= b  
FT /tag= c  
XX WO200123523-A2.  
PN 05-APR-2001.  
XX  
XX

PF 02-OCT-2000; 2000WO-US27202.  
XX  
PR 30-SEP-1999; 99US-0409634.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Kirst S, Wrighton N, Fraser CC;  
XX  
DR WPI; 2001-235372/24.  
XX P-PsDB; AAU00501.  
PT Isolated secreted proteins and their encoding nucleic acids are used  
PT for diagnosis and treatment of e.g. bacterial and viral infections,  
PT autoimmune diseases and inflammatory disorders -  
XX  
PS Claim 2; Fig 14; 261pp; English.  
XX  
CC The present sequence encoding for human TANGO 330 form 2 is  
CC isolated from cDNA clone Jthx181e12 from a human astrocyte cDNA  
CC library. TANGO 330 is 1 of 4 novel human transmembrane proteins  
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)  
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins  
CC are useful as modulating agents in regulating a variety of cellular  
CC processes and can be used to express the proteins in a host cell in  
CC gene therapy applications. Antisense nucleic acid molecules and  
CC expression vectors containing the TANGO nucleic acids are also described.  
CC Diagnostic assays can be used to detect genetic alterations in the TANGO  
CC nucleic acids and to identify compounds that bind to or modulate activity  
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to  
CC monitor protein levels in tissue as a clinical testing procedure.  
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids  
CC and proteins may be used to human Roundabout, treat and monitor disorders of the  
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They  
CC can also be used to treat cell proliferative disorders (e.g. cancer),  
CC and neurological disorders e.g. Alzheimer's disease.  
XX  
SQ Sequence 3808 BP; 773 A; 1244 C; 1041 G; 750 T; 0 other;  
Alignment Scores:  
Pred. No.: 3.14e-83 Length: 3808  
Score: 1453.00 Matches: 272  
Percent Similarity: 98.56% Conservative: 1  
Best Local Similarity: 98.19% Mismatches: 3  
Query Match: 90.36% Indels: 1  
DB: 22 Gaps: 0  
US-10-047-021-86 (1-303) x AAS01695 (1-3808)  
Qy 24 GlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAspGlnLeuPhe 43  
Db 171 GGAGGATGGCTCAGGACTCCCGCCCGCAGATCTTAGTCCACCCCGAGGACGAGTGTTC 230  
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProProThrIle 63  
Db 231 CAGGGCCCTGCGCTGCCAGGATGAGTGCAGGCTTCAGGCGCCAGCCACCTCCACCATC 290  
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisLeuLeu 83  
Db 291 CGCTGGTTGCTGAATGGGCAGCCCTGAGCATGGTGGCCCGCCAGACCCACACCATCTCTG 350  
Qy 84 ProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103  
Db 351 CCGTATGGGACCTTCTGTCTGCTACAGCCCTCGCCGGGGAGCATGCCACGATGCCAG 410  
Qy 104 AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla 123  
Db 411 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCGCAGCAACCGCTTGGCACGGCA 470  
Qy 124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143  
Db 471 GTCAGCAGAGCGCTCGGCTGTCTGTGGCTGTCTCGGGAGGATTTCCAGATCCAGCT 530  
Qy 144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163

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PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077751P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1998; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 98US-0254465.
PR 10-MAR-1999; 98US-0265686.
PR 12-APR-1999; 98US-0284291.
PR 14-MAY-1999; 98US-0311832.
PR 14-MAY-1999; 98US-0380137.
PR 25-AUG-1999; 98US-0380138.
PR 25-AUG-1999; 98US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.

PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
PR (GETH ) GENENTECH INC.
XX Ahkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D,
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB,
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Kijavini LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
XX P-PSDB; ABU61102.
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies -
XX Claim 2; Fig 76; 459pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC The present sequence encodes a human PRO polypeptide of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/patidentry.html.
XX SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 other;

Alignment Scores:
Pred. No.: 2.14e-89 Length: 3716
Score: 1550.00 Matches: 292
Percent Similarity: 98.65% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 3
Query Match: 96.39% Indels: 1
DB: 25 Gaps: 0

US-10-047-021-86 (1-303) x ABX92441 (1-3716)
Qy 4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuMet 23
Db 1 GGAGGACAGACCTCTCTGGGGGGGAGGGGTTCCTGCTGCTGCTGCTCATG 60
Qy 24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
Db 61 GGAGGACATGGCTCAGGACTCCCGCCCGAGATCTAGTCCACCCAGGACAGCTGTTTC 120
Qy 44 GlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProProThre 63
Db 121 CAGGGCCCTGGCCCTGCCAGATGAGCTGCGAACCTCAGGCCAGCACCTCCACCATC 180
Qy 64 ArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLeu 83
Db 181 CGCTGGTGTGATGATGGGACAGCCCTGAGGATGATGGTGGCCCGCCAGCACCATCTCTG 240
Qy 84 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
```





[illegible]



Pred. No.: 8.83e-90 Length: 4262  
Score: 1557.00 Matches: 294  
Percent Similarity: 98.33% Conservative: 1  
Best Local Similarity: 98.00% Mismatches: 4  
Query Match: 96.83% Indels: 1  
DB: 22 Gaps: 0

US-10-047-021-86 (1-303) x AAH18180 (1-4262)

```
QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
DB 40 ATGGGCTCTGGAGGAGACAGGCTCTCTGGGGGAGGGGTTCCTGCTCTCTCTCTG 99
QY 21 LeuileMetGlyGlyMetAlaGlnAspSerProGlnileLeuValHisProGlnAsp 40
DB 100 CTCATCATGGGAGGAGTGGCTCAGGACTCCCGCCGCCAGATCTTAGTCCACCCCGAGGAC 159
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
DB 160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCAGCCACT 219
QY 61 ProThrileArgTTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
DB 220 CCCACCATCCGCTGGTCTGAATGGGAGCCCTCGAGCATGGTCCCGCCAGACCCACAC 279
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
DB 280 CACCTCTCTGCTGATGGGACCTTCTGCTGTACAGCCCTGCGCGGGAGCATGCCAC 339
QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
DB 340 GATGCCAGGCGCTCTCCACAGCTGGTGTGTACACATGTGAGGCCAGCAACCGGCTT 399
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
DB 400 GGCACGGCAGTCAGCAGAGGGCGCTGGCTGTCTGTGGCTGCTCTCCGGAGGATTTCCAG 459
QY 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
DB 460 ATCCAGCTTCGAGACATGGTGGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGCG 519
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyLysProLeuAlaLeu 180
DB 520 CCCTGGGGCCACCCAGAGCCACAGCTCTCATGGTGAAGATGAGAAACCCCTGGCCCTC 579
QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
DB 580 CAGCCCGGAGGACACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGT 639
QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
DB 640 GACGAGGGGACCTACATGTGTGTGGCCACACAGCGCAGGACACAGGAGGAGCGCGCA 699
QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240
DB 700 GCGCGGGTTTCCATCCAGGAGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTG 759
QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
DB 760 CGAATTCAGCTGGAATATGTACATGTGTGAACCCCGGATCTCTGACAGGGGCCCCAAGCCT 819
QY 261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuTh 280
DB 820 AGACCGCGGTGTGGCTCAGCTGGAGAGTCACTGAGCGCTGTGCGCTGCCCATCTTAC 879
QY 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
DB 880 ACGGCTTTGTTCCAGGACCCAGACTGCCCGGAGGAGCCAGGAGCTCCGTTGGCAGAGG 937
```

## RESULT 6

AAH78073

ID AAH78073 standard; DNA; 4262 BP.

XX

```
AC AAH78073;
XX 26-NOV-2001 (first entry)
DT
XX Nucleotide sequence of a human protein kinase/protein phosphatase.
DE Human; protein kinase; protein phosphatase; signal transduction;
XX intracellular signalling pathway; ss.
KW Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 40..2418
XX FT /*tag= a
XX FT /product= "protein kinase/protein phosphatase"
XX
XX WO200109345-A1.
XX
XX 08-FEB-2001.
XX
XX 28-JUL-2000; 2000WO-JP05060.
XX
XX 29-JUL-1999; 99JP-0248036.
XX 18-OCT-1999; 99US-0159590.
XX 11-JAN-2000; 2000JP-0118776.
XX 17-FEB-2000; 2000US-0183322.
XX 02-MAY-2000; 2000JP-0183767.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX Senoo C, Nezu J;
XX
XX WPI; 2001-564736/63.
XX P-PSDB; AAG67430.
XX
XX New genes encoding protein kinase and protein phosphatase, useful for
XX identifying modulators which can be used to treat human or animal
XX disorders associated with the expression or function of these enzymes -
XX
XX Claim 1; Page 164-174; 336pp; Japanese.
XX
XX The present sequence encodes a human protein kinase/protein
XX phosphatase. The polypeptides are expected to participate in signal
XX transduction in cells. The kinase phosphatases are connected with
XX intracellular signalling pathways. Antisense oligonucleotides and
XX compounds identified by screening (agonists or antagonists) can be
XX used to treat human or animal disorders associated with the expression
XX or function of the protein. In addition, the polypeptides may be used
XX as target molecules for drug development.
XX
XX Sequence 4262 BP; 873 A; 1333 C; 1209 G; 847 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 8.83e-90 Length: 4262
XX Score: 1557.00 Matches: 294
XX Percent Similarity: 98.33% Conservative: 1
XX Best Local Similarity: 98.00% Mismatches: 4
XX Query Match: 96.83% Indels: 1
XX DB: 22 Gaps: 0
XX
XX US-10-047-021-86 (1-303) x AAH78073 (1-4262)
XX
XX QY 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20
XX DB 40 ATGGGCTCTGGAGGAGACAGGCTCTCTGGGGGAGGGGTTCCTGCTCTCTCTCTG 99
XX QY 21 LeuileMetGlyGlyMetAlaGlnAspSerProGlnileLeuValHisProGlnAsp 40
XX DB 100 CTCATCATGGGAGGAGTGGCTCAGGACTCCCGCCGCCAGATCTTAGTCCACCCCGAGGAC 159
XX QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
XX DB 160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCAAGCCTCAGGCGCAGCCACT 219
XX
XX 61 ProThrileArgTTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
XX DB 220 CCCACCATCCGCTGGTCTGAATGGGAGCCCTCGAGCATGGTCCCGCCAGACCCACAC 279
XX QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
XX DB 280 CACCTCTCTGCTGATGGGACCTTCTGCTGTACAGCCCTGCGCGGGAGCATGCCAC 339
XX QY 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
XX DB 340 GATGCCAGGCGCTCTCCACAGCTGGTGTGTACACATGTGAGGCCAGCAACCGGCTT 399
XX QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
XX DB 400 GGCACGGCAGTCAGCAGAGGGCGCTGGCTGTCTGTGGCTGCTCTCCGGAGGATTTCCAG 459
XX QY 141 IleGlnProArgAspMetValAlaValValGlyGlnGlnPheThrLeuGluCysGlyPro 160
XX DB 460 ATCCAGCTTCGAGACATGGTGGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGCG 519
XX QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyLysProLeuAlaLeu 180
XX DB 520 CCCTGGGGCCACCCAGAGCCACAGCTCTCATGGTGAAGATGAGAAACCCCTGGCCCTC 579
XX QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200
XX DB 580 CAGCCCGGAGGACACACAGTGTCCGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGT 639
XX QY 201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
XX DB 640 GACGAGGGGACCTACATGTGTGTGGCCACACAGCGCAGGACACAGGAGGAGCGCGCA 699
XX QY 221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240
XX DB 700 GCGCGGGTTTCCATCCAGGAGCCCGCAGGACTACAGGAGCCTGTGGAGCTTCTGGCTGTG 759
XX QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
XX DB 760 CGAATTCAGCTGGAATATGTACATGTGTGAACCCCGGATCTCTGACAGGGGCCCCAAGCCT 819
XX QY 261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuTh 280
XX DB 820 AGACCGCGGTGTGGCTCAGCTGGAGAGTCACTGAGCGCTGTGCGCTGCCCATCTTAC 879
XX QY 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
XX DB 880 ACGGCTTTGTTCCAGGACCCAGACTGCCCGGAGGAGCCAGGAGCTCCGTTGGCAGAGG 937
```

CC disease, or endometriosis by detecting the amount of ECSM4 present in  
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in  
CC gene therapy for treating a hypoxic condition such as cancer, cardiac  
CC disease, endometriosis or atherosclerosis and in the manufacture of  
CC medicaments for treating the above disease. The sequences are useful  
CC for modulating angiogenesis in an individual. The present sequence  
CC encodes human ECSM4 protein.

XX  
SQ Sequence 3715 BP; 725 A; 1239 C; 1053 G; 698 T; 0 other;

## Alignment Scores:

Pred. No.: 2,398-90 Length: 3715  
Score: 1565.00 Matches: 295  
Percent Similarity: 98.67% Conservative: 1  
Best Local Similarity: 98.33% Mismatches: 3  
Query Match: 97.33% Indels: 1  
DB: 24 Gaps: 0

US-10-047-021-86 (1-303) x ABK87137 (1-3715)

QY 1 MetGlySerGlyGlyValSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu 20  
DB 70 ATGGGCTCTGGAGGACAGCTCTCTGGGGGACGGGTTCCCTGCTGCTGCTCTG 129  
QY 21 LeuileMetGlyGlyMetAlaGlnAepSerProProGlnileLeuValHisProGlnAep 40  
DB 130 CTCATCATGGAGGATGCTCAGGACTCCCGCCGAGATCTAGTCCACCCCGAGGAC 189  
QY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
DB 190 CAGCTGTTCAGGGGCTTGGCCCTGCCAGGATGAGCTGCCAAGCCCTCAGGCCAGCCT 249  
QY 61 ProThrileArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80  
DB 250 CCCACATCCGCTGGTGTGATGGGAGCCCTGAGCATGCTGCCCGCCAGACCCACAC 309  
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuLeuProProAlaArgGlyHisAlaHis 100  
DB 310 CACCTCTGCTGATGGGACCTTCTGCTGTACAGCCCTGCGCGGGGACATGCCAC 369  
QY 101 AspGlyGlnAlaLeuSerThrAepLeuGlyValThrCysGluAlaSerAenArgLeu 120  
DB 370 GATGCCAGGGCTCTGCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTT 429  
QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAepPheGln 140  
DB 430 GGCACGGCAGTCAGCAGAGGCGCTCGGTGTCTGTGGTGTCTCCCGGGAGATTTCAG 489  
QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160  
DB 490 ATCCAGCTTCGGACATGCTGCTGTGGGTGAGCAGTTTACTCTGGATGTGGGCGG 549  
QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180  
DB 550 CCTCGGGGACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGCGCTC 609  
QY 181 GlnProGlyArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSer 200  
DB 610 CAGCCCGGAAGGCACACAGTGTCCCGGGGGTCCCTGCTGATGGCAGAGCAGAGAAGT 669  
QY 201 AspGlu\*\*\*ThrTyrMetCysValAlaThrAenSerAlaGlyHisArgGluSerArgAla 220  
DB 670 GACGAAGGGACCTACTATGTGTGGCCACCAACAGCGCAGGCATAGGAGAGCGCGCA 729  
QY 221 AlaArgValSerIleGlnGluProGlnAepTrpThrGluProValGluLeuLeuAlaVal 240  
DB 730 GCCCGGGTTTCCATCCAGAGGCCCGCAGACTACACGGAGCTGTGGAGCTTCTGGCTGT 789  
QY 241 ArgIleGlnLeuGluAsnValThrLeuLeuAenProAepProAlaGluGlyProLysPro 260  
DB 790 CGAATTCAGCTGGAAATGTGACACTGCTGAACCCGGATCTTCAGAGGGGCCCAAGCT 849  
QY 261 ArgProAlaValTrpLeu\*\*\*TrpLysValSerGlyPro\*\*\*ArgLeuProAsnLeuTh 280

DB 850 AGACGGCGGTGTGGCTCAGCTGGAAGGTCTAGTGGCCCTGCGCCATCTTAC 909  
QY 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
DB 910 ACGGCTTGTTCAGAGACCCAGACTGCCCGGGAGGCCAGGAGCTCCGTGGCAGAGG 967

## RESULT 5

AAH18180  
ID AAH18180 standard; cDNA; 4262 BP.

XX AAH18180;

AC AAH18180;  
DT 26-JUN-2001 (first entry)

XX Human cDNA sequence SEQ ID NO:18084.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Claim 8; SEQ ID 18084; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX Sequence 4262 BP; 873 A; 1333 C; 1209 G; 847 T; 0 other;

Alignment Scores:

XX An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis -  
PS Claim 1; SEQ ID NO 134; 509pp; English.  
XX The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat  
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions  
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC parkinson's disease. The present sequence is a coding sequence of the  
CC invention.

XX  
SQ Sequence 3267 BP; 628 A; 1101 C; 927 G; 611 T; 0 other;

#### Alignment Scores:

Pred. No.: 2,09e-90 Length: 3267  
Score: 1565.00 Matches: 295  
Percent Similarity: 98.67% Conservative: 1  
Best Local Similarity: 98.33% Mismatches: 3  
Query Match: 97.33% Indels: 1  
DB: 24 Gaps: 0

US-10-047-021-86 (1-303) x ABNS9723 (1-3267)

Qy 1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuLeuLeuLeu 20  
Db 35 ATGGGCTCTGGAGGAGACAGCTCTCTGGGGGAGGGGTTCCTGCTCTGCTCTG 94  
Qy 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProGlnLeuLeuValHisProGlnAsp 40  
Db 95 CTCATCATGGGAGGATGGCTCAGGACTCCCGCGCCAGATCTAGTCCACCCCGAGGAC 154  
Qy 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60  
Db 155 CAGCTGTTCAGGGCCCTGGCCCTGCGAGGATGAGTCCCAAGCTCAGGCCACCT 214  
Qy 61 ProThrLeuArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80  
Db 215 CCCACCATCCCTGGTGTCTGAATGGGAGGAGCCCTGAGCATGGTCCCGCCAGACCCACAC 274  
Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
Db 275 CACCTCTCTGCTGATGGGAGCCCTTCTGCTGTACAGCCCTGCGCGGGAGCATGCCAC 334  
Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsnArgLeu 120  
Db 335 GATGCCAGGGCCCTGTCCACAGACCTGGGTGTCTACATGTGAGGCCAGCAACCGGCTT 394  
Qy 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140  
Db 395 GGCACGGCAGTCAGCAGAGGCGCTCGGTCTGTGGGTCTCTCCCGGGAGGATTTCCAG 454  
Qy 141 IleGlnProArgAspMetValAlaValGlyGlnGlnPheThrLeuGluCysGlyPro 160  
Db 455 ATCCAGCCCTCGGAGCATGGTGGCTGTGGTGGTGGAGCAGTTTACTCTGGAATGTGGGCG 514  
Qy 161 ProTrpGlyHisProGluProThrValSerTrpTrpIleAspGlyIleProLeuAlaLeu 180  
Db 515 CCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGAAACCCCTGGCCCTC 574  
Qy 181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluIleSer 200  
Db 575 CAGCCCGGAGGACACAGTCTCCGGGGGGTCTCCCTGCTGATGGCAAGAGCAGAGAGAGT 634  
Qy 201 AspGlu\*\*\*\*ThrTyMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220  
Db 635 GACGAAGGGACCTCATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCGCGCA 694

Qy 221 AlaArgValSerIleGlnGluProGlnAspTyThrGluProValGluLeuLeuAlaVal 240  
Db 695 GCCGGGTTTCCATCCAGGAGGCCCCAGGACTACACGAGGAGCTGTGGAGCTTCTGGCTGTG 754  
Qy 241 ArgIleGlnLeuGluAenValThrLeuLeuAenProAspProAlaGluGlyProGlyPro 260  
Db 755 CGAATTCAGCTGGGAAATGTGACACTGCTGAACCCGGATCTGCGAGAGGGCCCCAAGCCT 814  
Qy 261 ArgProAlaValTrpLeu\*\*\*\*TrpIleValSerGlyPro\*\*\*\*ArgLeuProAenLeuTh 280  
Db 815 AGACCGCGGTGTGGCTCAGCTGGAAGGTCACTGGCGCTGCTGCGCTGCCCAATCTTAC 874  
Qy 280 rArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
Db 875 ACGGCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGAGGCTCCGTGGGCGAGAGG 932

#### RESULT 4

ABK87137  
ID ABK87137 standard; cDNA; 3715 BP.  
XX  
AC ABK87137;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE cDNA human ECSM4 protein.  
XX  
KW Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;  
KW imaging vascular endothelium; proliferative disease; cancer;  
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;  
KW endothelial damage; tumour neovasculature; cardiac disease;  
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;  
KW cardiant; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 70..3384  
FT /\*tag= a  
FT /product= "ECSM4"  
XX  
FN WO200236771-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 06-NOV-2001; 2001WO-GB04906.  
XX  
PR 06-NOV-2000; 2000US-245566P.  
PR 07-MAR-2001; 2001US-273662P.  
XX  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
XX  
PI Bicknell R, Huminiecki L;  
XX  
DR WPI; 2002-508120/54.  
XX  
DR P-PSDB; AAU99419.  
XX  
PT Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for  
PT imaging, diagnosing and treating a condition involving vascular  
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -  
XX  
PS Disclosure; Fig 12; 248pp; English.

XX The present invention relates to endothelial cell-specific molecule 4  
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4  
CC proteins are useful for imaging vascular endothelium in the body of  
CC an individual, and for diagnosing and treating a proliferative  
CC disease or condition involving the vascular endothelium (preferably,  
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,  
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in  
CC the manufacture of diagnostic or prognostic agent for such conditions.  
CC The proteins are also useful for detecting endothelial damage or  
CC activation, detecting a tumour or tumour neovasculature, cardiac



```
XX OS Homo sapiens.
XX PN WO9911293-A1.
XX PD 11-MAR-1999.
XX PF 03-SEP-1998; 98WO-US18360.
XX PR 12-SEP-1997; 97US-0058974.
XX PR 05-SEP-1997; 97US-0057626.
XX PR 05-SEP-1997; 97US-0057663.
XX PR 12-SEP-1997; 97US-0058666.
XX PR 12-SEP-1997; 97US-0058667.
XX PR 12-SEP-1997; 97US-0058973.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;
XX PI Rosen GA, Ruben SM, Shi Y;
XX DR WPI; 1999-204988/17.
XX DR P-PSDB; AAY12934.
XX PT New isolated human genes and the secreted polypeptides they encode
XX PT - useful for diagnosis and treatment of e.g. neurological disorders,
XX PT tumours, immune disorders, inflammation or haematological disorders
XX PS Claim 1; Page 165-166; 215pp; English.
XX CC AAX51701-55 encode human secreted proteins. The polynucleotides and
XX CC their corresponding secreted polypeptides are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g. by protein or gene
XX CC therapy. Pathological conditions can also be diagnosed by determining
XX CC the amount of the new polypeptides in a sample or by determining the
XX CC presence of mutations in the new polynucleotides. Specific uses are
XX CC described for each polynucleotide, based on which tissues they are
XX CC most highly expressed in, and include developing products for the
XX CC diagnosis or treatment of cancer, immune disorders, infection,
XX CC inflammatory disorders, skin disorders, tumours, atherosclerosis,
XX CC restenosis, autoimmune disorders, Alzheimer's disease, peripheral
XX CC neuropathies, trauma, spinal cord injuries, allergy, hematopoietic
XX CC disorders, skeletal disorders, neurological disorders, arthritic
XX CC disorders, asthma, immunodeficiency diseases, AIDS and transplant
XX CC rejection. The polypeptides are also useful for identifying their
XX CC binding partners.
XX SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 6 other;

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Score: 1602.00 Matches: 303
Percent Similarity: 100.00% Conservative: 0
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Query Match: 99.63% Indels: 0
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DB 91 CTCATCATGGAGGAGGATGGCTCAGGACTCCCGGCCCCAGATCTTAGTCCACCCCGGAGC 150
OY 41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
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211 CCCACCATCCGCTGGTGTGCTGAATGGCAGCCCTGAGCATGGTCCGCCAGACCCACAC 270
81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
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101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
331 GATGGCCAGGCCCTGTCTCCAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 390
121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
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161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
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571 CAGCCCGAAGGCACACAGTGTCCGGGGGTCCCTGCTGATGGCAGCAGAGAGAGT 630
201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
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301 AsnThrGly 303
931 AACACAGGA 939

RESULT 2
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ID ABQ92573 standard; cDNA; 1346 BP.
XX AC ABQ92573;
XX DT 12-NOV-2002 (first entry)
XX DE Human secreted protein encoding cDNA SEQ ID NO 31.
XX KW Human; neutrotropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX KW antiparkinsonian; antisickling; antianemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
XX KW gene; 88.
XX OS Homo sapiens.
XX PN WO200257420-A2.
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2004, 11:37:09 ; Search time 241.772 Seconds  
(without alignments)  
3393.062 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1602	99.6	1346	20	AA51721 DNA encoding a hum
2	1502	99.6	1346	24	AB092573 Human secreted pro
3	1565	97.3	3267	24	ABN59723 Novel human coding
4	1565	97.3	3715	24	ABK87137 cDNA human ECSM4 p
5	1557	96.8	4262	22	AAH18180 Human cDNA sequenc
6	1557	96.8	4262	22	AAH78073 Nucleotide sequenc
7	1550	96.4	3716	20	AAZ34069 Human PRO860 nucle
8	1550	96.4	3716	21	AAC78052 Human PRO860 (NQ4
9	1550	96.4	3716	25	ABX2441 cDNA encoding huma
10	1453	90.4	3808	22	AA501695 Human TANGO 330 fo
11	1190	74.0	756	22	AAH08234 Human cDNA clone (
12	1145.5	71.2	3688	24	ABK87138 cDNA mouse ECSM4 p
13	1104.5	68.7	3042	22	AA501694 Human TANGO 330 fo
14	453	28.2	4291	20	AAV69278 Human T85 cDNA. H
15	446.5	27.8	4956	20	AA557770 Human Robo 1 polyp
16	446.5	27.8	4956	20	AA57253 Human ROBO1 cDNA.
17	405	25.2	4188	20	AA55767 Drosophila Robo 1
18	405	25.2	4188	20	AA57250 Drosophila sp. ROB
19	405	25.2	4355	23	ABL22881 Drosophila melanog
20	404.5	25.2	6215	24	ABL49658 Human neurotransmi
21	396.5	24.7	6445	24	AA49652 Human neurotransmi
22	356.5	22.2	3894	20	AA55769 C. elegans Robo po
23	356.5	22.2	3894	20	AA57252 C. elegans ROBO cd
24	347	21.6	2499	23	ABL09471 Drosophila melanog
25	345	21.5	4146	20	AA55768 Drosophila Robo 2
26	345	21.5	4146	20	AA57251 Drosophila sp. ROB
27	311	19.3	232	21	AAZ42889 Human 5' EST isola
28	307	19.1	2658	23	ABL09371 Drosophila melanog
29	298.5	18.6	299	22	AA53325 Human cardiovascular
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35	276.5	17.2	5530	22	ABA08831 Human peroxidasin
36	276.5	17.2	6814	24	AB570409 Human bone remodel
37	276.5	17.2	6847	20	AAV99922 Melanoma associate
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39	275.5	17.1	4694	22	AA51847 Human polynucleoti
40	267.5	16.6	4080	25	AA49595 Human cytoskeleton
41	267.5	16.6	4131	25	ABT16046 NOVX related polyn
42	267.5	16.6	4360	25	AA49596 Human cytoskeleton
43	267.5	16.6	4739	22	AAK51848 Human polynucleoti
44	265.5	16.5	5093	24	AA139621 Human secreted pro
45	260	16.2	4548	24	AA164283 Human transient ax

ALIGNMENTS

RESULT 1

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ID AAX51721 standard; DNA; 1346 BP.

XX AC AAX51721;

XX AC AAX51721;

DT 17-JUN-1999 (first entry)

XX DNA encoding a human secreted protein.  
KW Human secreted protein; cancer; immune disorder; infection;  
KW inflammatory disorder; skin disorder; tumour; atherosclerosis;  
KW restenosis; autoimmune disorder; Alzheimer's disease;  
KW peripheral neuropathy; trauma; spinal cord injury; allergy;  
KW hematopoietic disorder; skeletal disorder; neurological disorder;  
KW arthritic disorder; asthma; immunodeficiency disease; AIDS;  
KW transplant rejection; ss.

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Weinstock,G. and Gibbs,R.A.  
Direct Submission  
Unpublished  
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Worley,K.C.  
Direct Submission  
Submitted (09-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
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Rat Genome Sequencing Consortium.  
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department  
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Baylor Plaza, Houston, TX 77030, USA  
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Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GRFO  
Center clone name: CH230-85A24  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 230810 bases at least Q40  
Consensus quality: 23159 bases at least Q30  
Consensus quality: 234781 bases at least Q20  
Estimated insert size: 236162; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: this is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have

## ----- Summary Statistics

Assembly program: Phrap; version 0.990329  
Consensus quality: 201827 bases at least Q40  
Consensus quality: 204782 bases at least Q30  
Consensus quality: 206701 bases at least Q20  
Estimated insert size: 209571; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

- \* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).
- \* NOTE: This is a 'working draft' sequence. It currently  
consists of 1 contigs. Gaps between the contigs  
are represented as runs of N. The order of the pieces  
is believed to be correct as given, however the sizes  
of the gaps between them are based on estimates that have  
been provided by the submitter.
- \* This sequence will be replaced  
by the finished sequence as soon as it is available and  
the accession number will be preserved.
- \* 1 223269: contig of 223269 bp in length.

## FEATURES

## source

1. 223269  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-136D4"  
478. .808  
/note="clone boundary  
clone\_end:Sp6  
site:  
end\_sequence: BH352255"  
104879. .106665  
/note="wgs contig"  
164341. .165851  
/note="wgs contig"  
204100. .207640  
/note="wgs contig"  
221935. .223269  
/note="wgs contig"

## misc\_feature

misc\_feature 59410 a 47952 c 46732 g 54018 t 15157 others

## misc\_feature

misc\_feature 104879. .106665

misc\_feature 164341. .165851

misc\_feature 204100. .207640

misc\_feature 221935. .223269

misc\_feature 221935. .223269

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misc\_feature 221935. .223269

misc\_feature 221935. .223269

## Alignment Scores:

Pred. No.: 3.12e-36 Length: 223269  
Score: 814.50 Matches: 208  
Percent Similarity: 37.08% Conservative: 23  
Best Local Similarity: 33.39% Mismatches: 49  
Query Match: 50.65% Indels: 344  
DB: 2 Gaps: 5

US-10-047-021-86 (1-303) x AC120636 (1-223269)

Qy 20 LeuLeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGln 39  
Db 202698 CTTTCCCTCTTAGGAGGAAGCTCTGGATTCTCCACCAGATCTAGTTTCATCCCCAG 202639  
Qy 40 AspGlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnPro 59  
Db 202638 GACCAAGTACTTCCGGGCTCCGGCCGGCCAGATGAGTTGAGAGCATCGGGCCCAACA 202579  
Qy 60 ProProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProAspPro 79  
Db 202578 CTTCCCACTATCCGCTGCTGTAATGGGAGCCCTCCAGATGGCCAGCCAGACCTA 202519  
Qy 80 HisHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAla 99  
Db 202518 CATTACCTCCAAATCAGATGGGACCTCTCTGTATACATCGGCCCTTACCCTAGGAGCGCG 202459  
Qy 100 HisAspGlyGln---AlaLeuSerThrAspLeuGlyValThrCysGluAlaSerAsn 118  
Db 202458 CAAGACACCAAGAAACATTTCTCTCAGCAATCTGGGTGTCATACATGTGAGGCGCAAC 202399  
Qy 119 ArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAla----- 133

Db 202398 CGGCTGGGCACAGCAGTGAAGCCGGGTGCTAGGCTGTCTGTGGC-TGGTGAGGCTTGGA 202340  
Qy 133 ----- 133  
Db 202339 GGGTAGGCTCAGGTGAGGAGGAGTGGCTAGGCTGCGATGTTTGTGTCCAAGGAATACAGG 202280  
Qy 133 ----- 133  
Db 202279 GTCTATCTATGAAGGAGGAGCCCGGTGCGGTCTTGGGATGAAGGTTAACTAGACATAAA 202220  
Qy 133 ----- 133  
Db 202219 CGGCAAGGAACCGGTACAGCAGAACTGGGTAGCGCTTAGGATAAGCAAGSACTCG 202160  
Qy 134 -----ValLeuArgGluAsp 138  
Db 202159 GGGTGGGTAGACATGCTTCTCTGTGATCCGCTGACCTCCCAATAGTCTCTCCAGAGGAC 202100  
Qy 139 PheGlnIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCys 158  
Db 202099 TTCCGATCCAACTCGGGACACAGTGGCGCTGGTGGCGAGAGCTTGGTTCTCGAGTGT 202040  
Qy 159 GlyProProTrpGlyHisProGluProThrValSerTrpTrpIysAspGlyLysProLeu 178  
Db 202039 GGTCTCTCCCTGGGCTACCCAAAGCCTTCACTCTCTGTGTGGAAAGATGGGAAACCCCTG 201980  
Qy 179 AlaLeuGlnProGlyArgHisThr----- 186  
Db 201979 GTCTCCAGCCAGGGAAGCGCACAGTGAAGCCCAATTCCTGGGAACTCTCTTTGTCC 201920  
Qy 186 ----- 186  
Db 201919 ATATATCATCTGTCTGGGCACATCAAGCAACTGACCCGCTCTCCAGTGGCATGTCCCT 201860  
Qy 186 ----- 186  
Db 201859 TGAAGATCTGAGGACAGGAGGCGCAAGAGACCTCAAAATGCCCTCCGCCCTCTAAGTTT 201800  
Qy 187 -----ValSerGlyGlySerLeuLeu 193  
Db 201799 CTCACACTGAAGATTTCATGGAGTATTTCAGCCCTGACAGGTGCTGGGATCTCTGTATG 201740  
Qy 194 MetAlaArgAlaGluLysSerAspGlu\*\*ThrTyrMetCysValAlaIleThrAsnSerAla 213  
Db 201739 GTGGCAAGAGCAGAGAAGAATGACACCGGGACCTATATGTGTATGSCCACCACCAATGCC 201680  
Qy 214 GlyHisArgGluSerArgAlaAlaArgValSerIleGln----- 226  
Db 201679 GGACACGGGAGAGTCGGGAGCCAGGCTGTCTATCCAGGGAAGGAGGAGTCACTA 201620  
Qy 226 ----- 226  
Db 201619 AAATCCAATAAGGCTCAGGAGATAACTCTGTGTGTAACTGCTTGCATATATATGTA 201560  
Qy 226 ----- 226  
Db 201559 AGACTCAAGCAGCCCGACCAATATAAAGCAGACTATGACAGTGTATGTTGATGATTC 201500  
Qy 226 ----- 226  
Db 201499 CAGTACAGCAAAATGTGGAGTACAGCAAGTGAATCCAGAAAGTAGCTAGACGCAAG 201440  
Qy 226 ----- 226  
Db 201439 TCTGCCAGTGGGTTCAGGTTTCAAGTTGTCTCAAAAAAACAAGATGGAGAACAGCAGT 201380  
Qy 226 ----- 226  
Db 201379 AAGGAGCTTTGGCTTCCATAGCCACGCTCACTCACTACATACACATGTGAACCCACT 201320  
Qy 226 ----- 226

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QY 226 ----- 226
D 187471 TGACAGTGAATGTCGATCATCCAGTGCAGTGTGGAGACAGACAGAGTGAATCCAGAA 187412
QY 226 ----- 226
D 187411 GCTAACACAGACAGTCTAGTCTACACAGTGAAGTTCACAGTTCAGTGAAGACCTGTGTCTCA 187352
QY 226 ----- 226
D 187351 AAAATAAGATAGAGATCAATAAATAGGAAGACTCTGTGTCAACGCTTACTACATAC 187292
QY 226 ----- 226
D 187291 ATGCATATAACACGCACTTAACCCACACTCAAGTTCAAGTAAAGTAGGAGACTCCA 187232
QY 226 ----- 226
D 187231 GTTAGTGTGGTCAACGAGTATGAGTGTGGGTCCCAAGTATGATGAGGCCCAATGGGCATAG 187172
QY 226 ----- 226
D 187171 GAATATCCAGAGCTGAATAACTCTGGGAGCCAAAGTTTCCACGATGAAGTAGTGTCTCA 187112
QY 227 ----- GluProGlnAspTyrThrGluProValG1 236
D 187111 CTACTCCATCCAGTCTGTGTCTCCACAGATCCAGACACACAGGACATCTAGA 187052
QY 236 uLeuLeuLaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaG1 256
D 187051 GCTTCTGCTGTGTTCGATTCAGTGGAAATGTGACCTCTGTAAACCCGACCTGTAAA 186992
QY 256 uGlyProLysProArgProAlaValThrLeu***TrrLys----- 269
D 186991 AGTCCCAAGCTGGGCCATCGTGTGCTCAGCTGGAAGGTGACAGAGGTCCAGAA 186932
QY 269 ----- 269
D 186931 AACCCACAGCTCAGATAGGGCTGCCATGAGTCCCTAGTCCATTATCGTGTCTGA 186872
QY 270 -----ValSerGlyPro***-ArgLeuProAsnLeuThrArgProCysSerGly 285
D 186871 CTCTTCCAGGTGAGCGGCCCTGTGTCAGCTCTGTGAGTCATACACAGCTCTGTTCAGGA 186812
QY 286 ProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
D 186811 CTCAGAGTCTCCCGAGGACCAAGGATCTCCATGGACAGAG 186770

RESULT 14
AC120636/c AC120636 223269 bp DNA linear HTG 20-NOV-2002
LOCUS Rattus norvegicus clone CH230-13604, *** SEQUENCING IN PROGRESS
DEFINITION
ACCESSION AC120636
VERSION AC120636.4 GI:25138029
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 223269)
Munzy,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Albrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleaveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,I.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
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Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Guregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, K., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Loulseg, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okunolu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plummer, F., Poindester, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 223269)  
Worley, K.C.  
Direct Submission  
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 223269)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Genome Center  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
Project Information  
Center project name: GXDD  
Center clone name: CH230-13604

Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
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 Project Information  
 Center project name: L28797  
 Center clone name: 356\_D\_13

----- Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 213654 bases at least Q40  
 Consensus quality: 213955 bases at least Q30  
 Consensus quality: 214104 bases at least Q20  
 Insert size: 210000; agarose-fp  
 Insert size: 214159; sum-of-contigs  
 Quality coverage: 10.7 in Q20 bases; agarose-fp  
 Quality coverage: 10.5 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 5437: contig of 5437 bp in length  
 \* 5438 5537: gap of 100 bp  
 \* 5538 134170: contig of 128633 bp in length  
 \* 134171 134270: gap of 100 bp  
 \* 134271 159037: contig of 24767 bp in length  
 \* 159038 159137: gap of 100 bp  
 \* 159138 212279: contig of 53142 bp in length  
 \* 212280 212379: gap of 100 bp  
 \* 212380 214559: contig of 2180 bp in length.

## FEATURES

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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="9"  
 /map="9"  
 /clone="RP23-356D13"  
 /clone\_lib="RPCI-23 Female Mouse BAC"  
 1. 5437  
 /note="assembly\_fragment"  
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 vector\_side:left  
 5538. 134170  
 /note="assembly\_fragment"  
 134271. 159037  
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 159138. 212279  
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 212380. 214559  
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 clone\_end:T7  
 vector\_side:right  
 BASE COUNT 57879 a 45778 c 47185 g 63317 t 400 others  
 ORIGIN

## Alignment Scores:

Pred. No.: 5,03e-38 Length: 214559  
 Score: 845.50 Matches: 208  
 Percent Similarity: 37.9% Conservative: 26  
 Best Local Similarity: 33.77% Mismatches: 46  
 Query Match: 52.58% Indels: 336  
 DB: 2 Gaps: 5

US-10-047-021-86 (1-303) x AC138284 (1-214559)

Qy 20 LeuLeuMetGlyGlyMetAlaGlnAaspSerProGlnIleLeuValHisProGln 39

Db 188611 CTTTCCTCTTAGGAGGTGAGGCTCTGGATCTCCACCCAGATCCTAGTTACCCCCAG 188552

Qy 40 AspGlnLeuPheGlnGlyProGlyProAlaArgMetSerCybArgAlaSerGlyGlnPro 59  
 Db 188551 GACCAGTACTTTCAGGGCTCTGGCCAGCCAGATGAGGTGCAGATCATCGGCCAACCA 188492  
 Qy 60 ProProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspPro 79  
 Db 188491 CCTCCCACTATCGCTGGCTGCTGAATGGGCAGCCCTCAGCATGGCCACCCAGACCTA 188432  
 Qy 80 HisHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAla 99  
 Db 188431 CATTACCTTTTGGCGGATGGACCCCTCTGTATCATCGGCCCTCTGTCCAGGAGCGGCCA 188372  
 Qy 100 HisAspGlyGln---AlaLeuSerThrAspLeuGlyValTyThrCysGluAlaSerAsn 118  
 Db 188371 CAAGATCACCAGAACATCCTCTCAGCAATCTGGGTCTCTACACATGTGAGCCAGCAAC 188312  
 Qy 119 ArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAla----- 133  
 Db 188311 CGGCTGGGCACAGCAGTGCAGCCGGGTGCTAGGCTGTCTGTGGCTGGTGGAGTGGAG 188252  
 Qy 133 ----- 133  
 Db 188251 GGTAGGCCAGGGGGAAGCAGAGTTAGGCTGAGATGCTTGTCTCAGGGAATAGCAGAG 188192  
 Qy 133 ----- 133  
 Db 188191 TCTGTCTGTGAGGGAGCAGGAGTCTGAGGCTTGGGATGGAGACTAGGTTAACTAG 188132  
 Qy 133 ----- 133  
 Db 188131 AGATAGAGGGGCAAGGAAGTGGTAGACAGAAATGGGTAAAGCATGTTCCGATAGCCATC 188072  
 Qy 133 ----- 133  
 Db 188071 CATGTTAGATGTTAGAAAGACTCAGGGTGGTAGACGTGCTTCTGCTGATTTGCTGAC 188012  
 Qy 134 -----ValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValVal 150  
 Db 188011 TTCCCAATAGTCTTCAGGAGGACTTCAGATCAACCTCGGACACAGTGGCGGTGTG 187952  
 Qy 151 GlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSer 170  
 Db 187951 GGAGAGAGCTTGGTTCCTTGTAGTGGTCTCTCCCTGGGGTACCCAAAACCTCGGTCTCA 187892  
 Qy 171 TrpTrpIleAspGlyHisProLeuAlaLeuGlnProGlyArgHis----- 185  
 Db 187891 TGGTGGAAAGACGGGAAACCCCTGCTCAGCCAGGGAGGCGCACAGTGAAGTGAACCC 187832  
 Qy 185 ----- 185  
 Db 187831 CAATCCTGGGNACTCCTTTGCCCATACATCATCCTGCTGGGCACATTGAGCACTGAC 187772  
 Qy 186 -----Thr 186  
 Db 187771 CCACCTCCAACTCTTAAGCTTCTCAAATTAAGACTTCATGGAGTATCTGAACCTGACA 187712  
 Qy 187 -ValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu\*\*\*ThrTyMe 206  
 Db 187711 GGTATCTGGGATTTCCCTGATGGTGTCAAGAGCAGAGAAGATGACTCGGGGACTATAT 187652  
 Qy 206 tCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleG1 226  
 Db 187651 GTGTATGCCCAACCAACAATGCTGGGCAACGGGAGCGGAGCAGCCAGGGGTGTCTATCCA 187592  
 Qy 226 n----- 226  
 Db 187591 GGGTAAGCAGCAGGAGTCTATCAATTAATTAAGGGCTCAGGAGAGAACTCTGTGGGTAA 187532  
 Qy 226 ----- 226  
 Db 187531 GGTGTGGCTTTCACATACGTGAAGAGTCAAGTTCTTCCAGCATCTCATATAAAGCAGAGTG 187472

Qy 171 TrpTtpLysAspGlyLysProLeuAlaLeuGlnProGlyArgHis----- 185  
Db 9511 TGGTGAAGAGCGGAAACCCCTGCTCCAGCCAGGAGCGCGAGTGAAGTGAACCC 9570  
Qy 185 ----- 185  
Db 9571 CAATCTGGGAACCTCTTTGGCCATACATCATCTGTCTGGGCACATTGAGCAACTGAC 9630  
Qy 186 -----Thr 186  
Db 9631 CCACCTTCAACCTTAAGCTTCTCAATTAAGACTTCATGGAGTATCTGAACCTGACA 9690  
Qy 187 -ValSerGlySerLeuLeuMetAlaGluLysSerAspGlu\*\*\*ThrTyrMe 206  
Db 9691 GGTATCTGGGATTCCTGTGAGTGTCAAGAGCAGAGAGATGACTCGGGGACCTATAT 9750  
Qy 206 tCysValAlaThrAenSerAlaGlyHisArgGluSerArgAlaAlaArgValSerIleG1 226  
Db 9751 GTGTATGGCCACCAACATGCTGGGCAACGGAGAGCGGAGCAGCGGTGTCTATCCA 9810  
Qy 226 n----- 226  
Db 9811 GGGTAAGCAGAGAGTCAATCTCAATCTAATAAGGGCTCAGAGAGAACTCTGTGGGTAA 9870  
Qy 226 ----- 226  
Db 9871 GGTGTGGCTTCACATACGTGAAGAGTCAAGTTCTCCAGCACTCATATAAAGCAGAGTG 9930  
Qy 226 ----- 226  
Db 9931 TGACAGTGAATGTCGATCATCCAGTCCAGTCCGATGTGGAGAACAGACAGAGTGAATCCAGAA 9990  
Qy 226 ----- 226  
Db 9991 GCTAACACAGACAGTCTAGTCTACACAGTGAAGTTCCAGTTCAGTGAAGACCTTGTCTCA 10050  
Qy 226 ----- 226  
Db 10051 AAAATAAGATAGATCAATAATAAGGAAGACTCTGTTCAACGGTTACTACATAC 10110  
Qy 226 ----- 226  
Db 10111 ATGCATATAAACACGCACTTAACCCACACACTCAAGTTCAAGTTAAGTAGGAGACTCCA 10170  
Qy 226 ----- 226  
Db 10171 GTTAGTGTGTCACAGGATATGAGTTTGGGTCCAGTTCAGTGATGAGGCCAAATGGGCATAG 10230  
Qy 226 ----- 226  
Db 10231 GAATACTCCAGAGTGAATACTCTGGGAGCCAAAGTTTCCACAGATGAAGTATGTTCCA 10290  
Qy 227 -----GluProGlnAspTyrThrGluProValG1 236  
Db 10291 CTACTCCATCCAGTCTGTGTTCTCCACAGAAATCCAGCAACCCACAGGAACATCTAGA 10350  
Qy 236 uLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaG1 256  
Db 10351 GCTTCTGGCTGTTCGATTCAGTTCAGTGGAAAAATGTGACCTGTCTAAACCCGCAACCTGTAA 10410  
Qy 256 uGlyProLysProArgProAlaValTIPLeu\*\*\*TIPlys----- 269  
Db 10411 AGGTCCCAAGCTGGGCCATCGGTGTGCTCAGCTGGGAAGGTGAGACAGAGGTCCAGAA 10470  
Qy 269 ----- 269  
Db 10471 AACACCCAGAGCTCAGATTAGGGCTGCCATGAGCTCCCTAGTCCATTATGTTGCTCTGA 10530  
Qy 270 -----ValSerGlyPro\*\*\*-ArgLeuProAsnLeuThrArgProCysSerGly 285  
Db 10531 CTTCTTCCAGGTGAGCGGCCCTGCTGCACCTGCTGAGTCAATACACAGCTCTGTTTCAGGA 10590

Qy 286 ProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
Db 10591 CTCAGAGTCCCCCGGAGCACCAGGATCTCCATGCACAGAGG 10632  
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AC138284  
DEFINITION  
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SEQUENCE, 5 unordered pieces.  
AC138284  
AC138284.3 GI:29164640  
VERSION  
HTG; HTGS PHASE1; HTGS DRAFT.  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1. (bases 1 to 214559)  
Birren,B., Nusbaum,C. and Lander,E.  
Mus musculus chromosome 9, clone RP23-356D13  
Unpublished  
2. (bases 1 to 214559)  
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barna,N., Baetien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,  
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,  
Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,  
Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,  
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,  
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,  
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R.,  
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,  
Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,  
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3. (bases 1 to 214559)  
Anderson,S., Arachchi,H.M., Barna,N., Baetien,V., Bloom,T.,  
Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,  
Collymore,A., Cooke,P., Cooke,P., Corum,B., DeArellano,K.,  
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,  
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,  
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,  
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
Rachupka,A., Ramasamy,J., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,  
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,  
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (23-MAR-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 23, 2003 this sequence version replaced gi:28460994.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://fcp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR



Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasiliiev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 4, 2003 this sequence version replaced gi:28201704.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIGR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submission@genome.wi.mit.edu](mailto:sequence_submission@genome.wi.mit.edu)

----- Project Information

Center project name: L19390

Center clone name: 325\_P\_4

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 206525 bases at least Q40

Consensus quality: 207512 bases at least Q30

Consensus quality: 207947 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 208212; sum-of-contigs

Quality coverage: 11.1 in Q20 bases; agarose-fp

Quality coverage: 9.7 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 38270: contig of 38270 bp in length  
\* 38271 38270: gap of 100 bp  
\* 38371 39590: contig of 1220 bp in length  
\* 39591 39690: gap of 100 bp  
\* 39691 47174: contig of 7484 bp in length  
\* 47175 47274: gap of 100 bp  
\* 47275 61618: contig of 14344 bp in length  
\* 61619 61718: gap of 100 bp  
\* 61719 86099: contig of 24381 bp in length  
\* 86100 86199: gap of 100 bp  
\* 86200 112506: contig of 26307 bp in length  
\* 112507 112607: gap of 100 bp  
\* 112607 143181: contig of 30575 bp in length  
\* 143182 143281: gap of 100 bp  
\* 143282 179163: contig of 35882 bp in length  
\* 179164 179263: gap of 100 bp  
\* 179264 209012: contig of 29749 bp in length.

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Score: 845.50 Matches: 208  
Percent Similarity: 37.99% Conservative: 26  
Best Local Similarity: 33.77% Mismatches: 46  
Query Match: 52.58% Indels: 336  
DB: 2 Gaps: 5

US-10-047-021-86 (1-303) x AC105958 (1-209012)

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Qy 80 HisHisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAla 99  
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Qy 151 GlyGluGlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSer 170  
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BASE COUNT 987 A 1446 C 1251 G 1010 T  
ORIGIN

Alignment Scores:  
Pred. No.: 1.96e-43 Length: 4694  
Score: 912.00 Matches: 186  
Percent Similarity: 62.00% Conservatives: 0  
Best Local Similarity: 62.00% Mismatches: 3  
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US-10-047-021-86 (1-303) x AK074163 (1-4694)

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QY 21 LeuLeuMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
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DB 69 ----- 69
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DB 69 ----- 69
QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
DB 69 ----- 69
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QY 121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
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QY 141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
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QY 161 ProTrpGlyHisProGluProThrValSerTrpTrpTplsAspGlyLysProLeuAlaLeu 180
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RESULT 12

AC105958

LOCUS

DEFINITION

AC105958

AC105958.6 GI:28827995

HTG; HTGS PHASE1; HTGS DRAFT.

Mus musculus (house mouse)

Mus musculus

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 209012)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhalter,B.,

Brown,A., Camarata,J., Campiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Collings,S., Collins,S., Collymore,A., Cook,A.,

Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,

Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

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Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,

Jones,C., Katat,A., Karatas,A., Kellis,C., LaRocque,K.,

Lamaze,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,

MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

McCarthy,M., McSwan,P., McKernan,K., McPheeters,R., Meldrim,J.,

Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,

Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,

Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,

Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,

Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

Viell,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (11-JAN-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 209012)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,

Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,

Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,

Collings,S., Collum,B., Corum,B., DeArellano,K., Faro,S.,

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Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,

Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,

Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,

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Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,

Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,

O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,

Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,

KEYWORDS  
SOURCE ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REMARK  
COMMENT

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 3467)  
Direct Submission  
Submitted (01-OCT-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline  
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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ORIGIN

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Query Match: 69.71% Indels: 1  
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US-10-047-021-86 (1-303) x BC014995 (1-3467)

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Qy 283 sSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299  
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RESULT 11  
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ACCESSION AK074163  
VERSION AK074163.1 GI:18676673  
KEYWORDS fis (full insert sequence).  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NEO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert and 5'- &  
3'-end one pass sequencing; Research Association for Biotechnology;  
cDNA library construction and clone selection; Kazusa DNA Research  
Institute.  
Location/Qualifiers  
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Qy 269 ----- 269
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Db 30846 GGGTAAAGCCGATCCAGAGCTCAAGAAAGGCGTTCCTGAGCTCTCTGACCCCGCGCC 30787
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Qy 270 -----ValSerGlyPro***ArgLeuProLeuThrArgPr 282
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Db 30786 TTCTCGAAACTCTTCCAGAGTCAGTGGCCCTGCTGCGCTGCGCAATCTTACAGGCC 30727
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Qy 282 cysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArg 299
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Db 30726 TTGTTCCAGACCCAGACTGCCCGCGGAGCCAGGAGCTCGTGGGCAGAGG 30675
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RESULT 8
BD150226 756 bp DNA linear PAT 17-JAN-2003
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION
ACCESSION BD150226
VERSION BD150226.1 GI:27855984
KEYWORDS JP 2002191363-A/5069.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patient: JP 2002191363-A 5069 09-JUL-2002;
COMMENT HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/5069
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC

C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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Location/Qualifiers
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Score: 1190.00 Matches: 232
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Best Local Similarity: 97.07% Mismatches: 6
Query Match: 74.00% Indels: 2
DB: 6 Gaps: 0

US-10-047-021-86 (1-303) x BD150226 (1-756)

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Qy 21 LeuIleMetGlyGlyMetAlaGlnAspSerProGlnIleLeuValHisProGlnAsp 40
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LOCUS Rattus norvegicus ROBO4 (Robo4) mRNA, complete cds.
DEFINITION
ACCESSION AY277635
VERSION AY277635.1 GI:30575794
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2886)
AUTHORS Roberts,K.G. and Stewart,L.M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2003) CRT Development Laboratory, Cancer Research
Technology, Suite 23, Dominion House, 59 Bartholomew Close, London,
England EC1A 7BE, United Kingdom
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source
1. .2886
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LOCUS AP003501 186971 bp DNA linear PRI 08-MAR-2002  
DEFINITION Homo sapiens genomic DNA, chromosome 11q, clone:RP11-664121,  
complete sequence.  
ACCESSION AP003501  
VERSION AP003501.2 GI:19263048  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE Homo sapiens genomic DNA  
JOURNAL Published Only in Database (2001)  
REFERENCE 2 (bases 1 to 186971)  
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,  
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (11-APR-2001) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suihoro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: hattori@isc.riken.go.jp, URL: http://hgp.riken.go.jp/  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT On Mar 7, 2002 this sequence version replaced gi:13603460.  
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Score: 1262.00 Matches: 277  
Percent Similarity: 48.44% Conservative: 3  
Best Local Similarity: 47.92% Mismatches: 16  
Query Match: .78.48% Indels: 283  
DB: 9 Gaps: 5  
US-10-047-021-86 (1-303) x AP003501 (1-186971)  
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Qy 83 LeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGly 102  
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Qy 133 ----- 133  
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Qy 187 ----- 187  
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Db 31506 CATCTCCGGTAGAATTGTGAGAGGGAGAGAGGGGGCTCAAACCTTCCCCCGAGTCA 31447  
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Db 31446 GAGCCCTCCCCACATAGGAGACTTTCAGTGAACCTGGGCCCTGACAGGTGTCCGGGGG 31387  
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Db	820	AGACCGGGGGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCGCCCTGCCCAACTTAC	879
Oy	280	TArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuAurGlyGlnArg	299
Db	880	ACGGCTTGTTCCAGGACCCAGACTGCCCCGGAGGCCAGGAGCTCCGTGGGCAAGG	937
RESULT 6			
LOCUS	AK027852		
DEFINITION	Homo sapiens CDNA FLJ14946 f16, clone PLACE2000034, weakly similar		
ACCESSION	AK027852		
VERSION	AK027852.1		
KEYWORDS	GI:14042831		
SOURCE	oligo capping; full (full insert sequence).		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 Isogai, T., Oca, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,		
JOURNAL	Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H.,		
REFERENCE	Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K.,		
AUTHORS	Arita, M., Nabokura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J.,		
TITLE	Makamatsu, A., Nakamura, Y., Nagahata, K., Masuno, Y. and Oshima, A.		
JOURNAL	NEDO human cDNA sequencing project		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 4262)		
TITLE	Isogai, T. and Otsuki, T.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,		
AUTHORS	Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 297-0812, Japan		
TITLE	(E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)		
JOURNAL	NEDO human cDNA sequencing project supported by Ministry of		
REFERENCE	Economy, Trade and Industry of Japan; cDNA full insert sequencing;		
AUTHORS	Research Association for Biotechnology; cDNA library construction,		
TITLE	5'- & 3'- and one pass sequencing and clone selection; Helix		
JOURNAL	Research Institute (supported by Japan Key Technology Center etc.)		
REFERENCE	and Department of Virology, Institute of Medical Science,		
AUTHORS	University of Tokyo.		
FEATURES	Location/Qualifiers		
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	RAARVSIQPDYTPREPVLLAVRIQLENVTLINPDPAKPKRPVWLTSMYSGPAA		
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	SNVLLRLPEKVPSPQEVTLKPGNGTVFVSWPVPENNHGIIKGYVSLNGTSTIS		
	PEPMATVVGEOPTQLIATHMPSYCVQAAVYAGAGSPSPVCLLEQAMERATQOE		
	SEHWGPTLEQLATLKEPREVATCGVALMLLLGLTAVICIHRRRARVHLGGLYATYS		
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	SRSPPVLLPPTSTFGYSLAEIPSTPARSPDPVAPRLPPLQALSSCCSSDS		
	CSRRSLSSPRLSLAARAAKAKKQELPHANSPLRLSHSTSLTAPACTIGRGSNTLS		
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ORIGIN			847 t

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Pred. No.:	2,016-80
Score:	1557.00
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Best Local Similarity:	98.00%
Query Match:	96.83%
DB:	9
Length:	4262
Matches:	294
Conservative:	1
Mismatches:	4
Indels:	1
Gaps:	0

US-10-047-021-86 (1-303) x AK027852 (1-4262)

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Db	100	CTCATCATGGAGGCAATGGCTCATGAGACTCTCCCGCCCGAGATCTTAAGTCAACCCCAAGAC	159
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Db	160	CAGTGTTCAGGGGCCCCCTGACCTCGCAGAGATGAGCTCCAAAGCTCAAGGCACACACT	219
QY	61	ProThr11earG1rPleuLeuAnaG1yG1nProleuSerMetValProProAspProHis	80
Db	220	CCCAACATCCGCTGGTGTGCTGAATGGGCAAGCCCCCGACATAGTGTCCCCCAAGACCAACAC	279
QY	81	HisLeuLeuProAspG1yThy1rleuLeuLeuLeuG1nProPro1a1aYag1yHis1aHis	100
Db	280	CACCTCTGCTGATGAGGACCTCTGCTGCTACAGCCCCCTGCCCCGGGGACATGGCCAC	339
QY	101	AspG1yG1n1a1aLeuSerThyAspLeuG1yVal1YrThrCySG1a1aSerASarXLeu	120
Db	340	GATGGCCAGGCTCTGTCCACAGACTGGGTGTCTACATGTGAGCCGACACCGGCTT	399
QY	121	G1YThr1a1aValSerArgG1y1a1aYrLeuSerVal1a1aValLeuArgG1uAspPheG1n	140
Db	400	GGCAGCGGCACTGACAGAGAGCCCTGGCTGTGTGGCTGTCTCCCGGAGAGATTCCAG	459
QY	141	11eG1nProAspAspMetVal1a1aVal1aG1yG1uG1nPhMetThrLeuG1nCyG1yPro	160
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Db	520	CCCTGGGGGCCACCCAGAGCCCAAGCTCATGTGTGAAGATGAGAAACCCCTGGCCCTC	579
QY	181	G1nProG1yArgHisThyValSerG1yG1ySserLeuLeuMet1a1aYr1aG1u1ySer	200
Db	580	CAGCCCGGAGGACACAGTGTCTCGGGGGGTCTCCGTGATGGCAAGCAGAGAAAGT	639
QY	201	AspG1u1**Thy1rMetCySVal1a1aThrAsnSer1aG1yHisArgG1uSerArg1a	220
Db	640	GACGAGGAGCACTCACTGTGTGTGGCCACCAACAGCAGACAGACAGGAGAAAGCCGCGCA	699
QY	221	AlaArgValSer11eG1nG1uProG1nAsp1YrThrG1uProVal1G1uLeuLeu1aVal	240
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QY	241	Arg11eG1nLeuG1uAsnValThy1rLeuLeuAsnProAspPro1a1aG1uG1yPro1yPro	260
Db	760	CGAATTACGTGAAATATGTGACACTGTGAACCCGATCTCTGACAGAGAGGCCCAAGCTT	819
QY	261	ArgPro1a1a1rPleu1**TrP1yValSerG1yPro1**ArgLeuProAsnLeuTh	280
Db	820	AGACCGCGGGTGTGGCTGACGTGAAGTCAATGGCCCTGCGCGGCTCGCCCAATCTTTAC	879
QY	280	1aYrArgProCySserG1yProArgLeuProArgG1u1a1aArg1uLeuArgG1yG1nArg	299
Db	880	ACGGCTCTTTGTTCAGAACCAAGACTGCCCCGGAGAGCCAGGAGCTCTCGTGGCAGAGG	937

RESULT 7  
AP003501/c



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 Qy 81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
 Db 280 CACCTCTGCTGCTGATGGAGCCCTTCTGCTGCTACAGCCCCCTGCCCCGGGAGCATGCCAC 339  
 Qy 101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGlnAlaSerAsnArgLeu 120  
 Db 340 GATGGCCAGGCGCTGCTCCAGACCTGGGCTGCTCTACATGATGAGGCCAGAACCGGCTT 399  
 Qy 121 GYTHRAAlaValSerArgGlyValAlaArgLeuSerValAlaValLeuArgGlnAspPheGln 140  
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 Db 460 ATCCAGCCTCGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
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 Db 580 CAGCCCGGAGGACACAGCTGCTCCGGGGGCTCCCTGCTGATGACAGACAGACAGAGACT 639  
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 Db 640 GACGAAAGGACCTTCACTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699  
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 LOCUS BDI60172  
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
 ACCESSION BDI60172  
 VERSION BDI60172.1 GI:27865930  
 KEYWORDS JP 2002191363-A/15015  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
 1 (bases 1 to 4262)  
 Ota,T., Isegai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,  
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.  
 Primer for synthesizing full-length cDNA and use thereof  
 Patent: JP 2002191363-A 15015 09-JUL-2002;  
 HELIX RESEARCH INSTITUTE  
 COMMENT  
 OS Homo sapiens (human)  
 PN JP 2002191363-A/15015  
 PD 09-JUL-2002  
 PF 28-JUL-2000 JP 200280990  
 PI TOSHIO OTA, TAKAO ISEGA, TETSUO NISHIKAWA, KOJI HAYASHI, KAZUO  
 PI SAITO  
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
 PI KEIICHI NAGAI, TETSUJI OTSUKI  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC

10,  
 PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
 Primer for synthesizing full-length cDNA and use thereof FH Key  
 Location/Qualifiers  
 FT CDS Location/Qualifiers  
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 BASE COUNT 873 a 1333 c 1209 g 847 t  
 ORIGIN  
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 Pred. No.: 2,01e-80 Length: 4262  
 Score: 1557.00 Matches: 294  
 Percent Similarity: 98.33% Conservative: 1  
 Best Local Similarity: 98.00% Mismatches: 4  
 Query Match: 96.83% Indels: 1  
 DB: Gaps: 0  
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 Qy 141 IleginProArgAspMetValAlaValAlaGlyGlnGlnPheThrLeuGlnCysGlyPro 160  
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Pred. No.: 6,38e-81 Length: 3872  
Score: 1565.00 Matches: 295  
Percent Similarity: 98.67% Conservative: 1  
Best Local Similarity: 98.33% Mismatches: 3  
Query Match: 97.33% Indels: 1  
DB: 9 Gaps: 0

US-10-047-021-86 (1-303) x AF361473 (1-3872)

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Db 190 CAGCTGTTCCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 249  
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QY 81 HisLeuLeuProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100  
Db 310 CACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369  
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QY 201 AspGlu\*\*\*ThrTyrMetCysValaValaValaValaValaValaValaValaVala 220  
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## RESULT 4

BD012213

## LOCUS

BD012213

4262 bp DNA linear PAT 02-AUG-2002

## DEFINITION

Novel genes encoding protein kinase or protein phosphatase.

## ACCESSION

BD012213.1 GI:22092402

## VERSION

WO 0109345-A/11.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Iehi, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T., Funahashi, S., Seno, C. and Nezu, J.

## AUTHORS

Novel genes encoding protein kinase or protein phosphatase

## TITLE

Patent: WO 0109345-A 11 08-FEB-2001;

## JOURNAL

HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOKYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUO NISHIKAWA, SHINICHI FUNAHASHI, HIROKI SENO, JUNICHI NEZU

## COMMENT

OS Homo sapiens (human)  
PN WO 0109345-A/11  
PD 08-FEB-2001  
PR 29-JUL-1999 JP 99P 248036, 11-JAN-2000 JP 00P 118776 PR  
17-FEB-2000 US 60/183322  
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUO NISHIKAWA, SHINICHI FUNAHASHI, CHIYAKI SENO, PI JUNICHI NEZU

## FEATURES

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## ORIGIN

US-10-047-021-86 (1-303) x BD012213 (1-4262)

## Alignment Scores:

Pred. No.: 2.01e-80 Length: 4262  
Score: 1557.00 Matches: 294  
Percent Similarity: 98.33% Conservative: 1  
Best Local Similarity: 98.00% Mismatches: 4  
Query Match: 96.83% Indels: 1  
DB: 6 Gaps: 0

## LOCUS

BD012213

## DEFINITION

Novel genes encoding protein kinase or protein phosphatase.

## ACCESSION

BD012213.1 GI:22092402

## VERSION

WO 0109345-A/11.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Iehi, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T., Funahashi, S., Seno, C. and Nezu, J.

## AUTHORS

Novel genes encoding protein kinase or protein phosphatase

## TITLE

Patent: WO 0109345-A 11 08-FEB-2001;

## JOURNAL

HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOKYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUO NISHIKAWA, SHINICHI FUNAHASHI, CHIYAKI SENO, PI JUNICHI NEZU

## COMMENT

OS Homo sapiens (human)  
PN WO 0109345-A/11  
PD 08-FEB-2001  
PR 29-JUL-1999 JP 99P 248036, 11-JAN-2000 JP 00P 118776 PR  
17-FEB-2000 US 60/183322  
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUO NISHIKAWA, SHINICHI FUNAHASHI, CHIYAKI SENO, PI JUNICHI NEZU

## FEATURES

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## BASE COUNT

873 a 1333 c 1209 g 847 t

## ORIGIN

US-10-047-021-86 (1-303) x BD012213 (1-4262)

## Alignment Scores:

Pred. No.: 2.01e-80 Length: 4262  
Score: 1557.00 Matches: 294  
Percent Similarity: 98.33% Conservative: 1  
Best Local Similarity: 98.00% Mismatches: 4  
Query Match: 96.83% Indels: 1  
DB: 6 Gaps: 0

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BD012213

## DEFINITION

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## ACCESSION

BD012213.1 GI:22092402

## VERSION

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## KEYWORDS

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## SOURCE

Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Iehi, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T., Funahashi, S., Seno, C. and Nezu, J.

## AUTHORS

Novel genes encoding protein kinase or protein phosphatase

## TITLE

Patent: WO 0109345-A 11 08-FEB-2001;

## JOURNAL

HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOKYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUO NISHIKAWA, SHINICHI FUNAHASHI, CHIYAKI SENO, PI JUNICHI NEZU

## COMMENT

OS Homo sapiens (human)  
PN WO 0109345-A/11  
PD 08-FEB-2001  
PR 29-JUL-1999 JP 99P 248036, 11-JAN-2000 JP 00P 118776 PR  
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PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUO NISHIKAWA, SHINICHI FUNAHASHI, CHIYAKI SENO, PI JUNICHI NEZU

## FEATURES

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## BASE COUNT

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## ORIGIN

US-10-047-021-86 (1-303) x BD012213 (1-4262)

## Alignment Scores:

Pred. No.: 2.01e-80 Length: 4262  
Score: 1557.00 Matches: 294  
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Query Match: 96.83% Indels: 1  
DB: 6 Gaps: 0

## LOCUS

BD012213

## DEFINITION

Novel genes encoding protein kinase or protein phosphatase.

## ACCESSION

BD012213.1 GI:22092402

## VERSION

WO 0109345-A/11.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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BASE COUNT 628 a 1101 c 927 g 611 t

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Pred. No.:	5,41e-81	Length:	3267
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Percent Similarity:	98.67%	Conservative:	1
Best Local Similarity:	98.33%	Mismatches:	3
Query Match:	97.33%	Indels:	1
DB:	6	Gaps:	0

US-10-047-021-86 (1-303) x AK405719 (1-3267)

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RESULT 3

AF361473

LOCUS

DEFINITION

AF361473

ACCESSION

AF361473.1 GI:16930357

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 3872)

Huminiack, L. and Bicknell, R.

In silico cloning of novel endothelial-specific genes

JOURNAL

MEDLINE

PUBMED

20530916

11076864

2 (bases 1 to 3872)

Huminiack, L. and Bicknell, R.

Direct Submision

TITLE

JOURNAL

Submitted (15-MAR-2001) ICRF, Institute of Molecular Medicine, John Radcliffe Hospital, Oxford OX3 9DS, UK

FEATURES

source

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DEFINITION	50 human secreted proteins.				
ACCESSION	BD074325				
VERSION	BD074325.1 GI:22619928				
KEYWORDS	JP 2001514024-A/30.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Moore, P.A., Ruben, S.M., Lafleur, D.W., Shi, Y., Rosen, C.A., Oleen, H.S., Ebner, R. and Brewer, L.A.				
TITLE	50 human secreted proteins				
JOURNAL	Patent: JP 2001514024-A 30 11-SEP-2001;				
COMMENT	HUMAN GENOME SCIENCES INC OS Homo sapiens (human) PN JP 2001514024-A/30 PD 11-SEP-2001 PF 03-SEP-1998 JP 2000508394 PR 05-SEP-1997 US 60/057626, 05-SEP-1997 US 60/057663 PR 05-SEP-1997 US 60/057669, 12-SEP-1997 US 60/058667 PR 12-SEP-1997 US 60/058974, 12-SEP-1997 US 60/058973 PR 12-SEP-1997 US 60/058666 PI PAUL A MOORE, STEVEN M RUBEN, DAVID W LAFLEUR, YANGU SHI, CRAIG A				
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ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1		
TITLE	Tang, Y.-T., Liu, C., Zhou, P., Asundi, V., Zhang, D., Zhao, Q. A., Ren, F., . . . Xue, A.-J., Yang, Y., Wehtman, T. and Dimañac, R. T.		
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GenCore version 5.1.6  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
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APPLICANT: Botstein, David  
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APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.

APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C65  
CURRENT APPLICATION NUMBER: US/09/999,833A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918595  
PRIOR FILING DATE: 2001-07-30  
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; PRIOR APPLICATION NUMBER: 60/085697  
  
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Best Local Similarity 98.8%; Pred. No. 4.1e-101;  
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
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Db 1 MCGWAQDSPPQILVHPDQQLFQGGPARMSCRAGQPPPTIRWLLNGQPLSMVPPDPHLL 60  
  
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Db 61 LPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRGLGTAVSRGARLSVAVLREDFQIQ 120  
  
Qy 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWMKDGKPLALQPGRHTVSGSLLMARAESKDE 202  
Db 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWMKDGKPLALQPGRHTVSGSLLMARAESKDE 180  
  
Qy 203 XYTMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 262  
Db 181 GTYMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRP 240  
  
Qy 263 AVMLXKXVSGP 273  
Db 241 AVMLXKXVSGP 251  
  
RESULT 14  
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; Sequence 211, Application US/09999833A  
; Publication No. US20030054405A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey



1	PRIOR FILING DATE: 1998-04-15	
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;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337; DB 11; Length 985;

Best Local Similarity 98.8%; Pred. NO. 4.1e-101;  
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 MCGMAQDSPPQILVHPQDOLFQCGCPARMSCOASGQPPPTIRWLNGOPLSMVPPDPHLL 60  
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DB 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHTVSGSLLMARAEKSDE 180  
QY 203 XYTCVATNSAGHRESRAARVSIQEPQDYTFEVELLAVRIQLENTVLNPDPAEGKPRP 262  
DB 181 GTYMCVATNSAGHRESRAARVSIQEPQDYTFEVELLAVRIQLENTVLNPDPAEGKPRP 240  
QY 263 AVLXWKVSGP 273  
DB 241 AVLXWKVSGP 251

RESULT 12

US-09-978-403A-211  
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; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
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; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: ROY, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C17  
; CURRENT APPLICATION NUMBER: US/09/978,403A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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Db 121 PRDVAVGEFTLECGPWGHPPTVSWKDGKPLAQGRHTTVSGSLIMARAESDE 180  
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Db 181 GTYMCVATNSAGHRESRAARVSIQBPQDYTBPVVELLAVRIQLENVTLNPDPAEGPKPRP 240  
QY 263 AVLWKVSGP 273  
Db 241 AVLWSKVSOP 251

RESULT 11  
US-09-978-191A-211  
; Sequence 211, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C4  
; CURRENT APPLICATION NUMBER: US/09/978,191A  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13  
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; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22



QY 23 MCGMAQDSPPQILVHPDQLFQGGPARMSCASQPPPTIRWLLNGQPLSNVPPDPHLL 82  
DB 1 MCGMAQDSPPQILVHPDQLFQGGPARMSCASQPPPTIRWLLNGQPLSNVPPDPHLL 60  
QY 83 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 142  
DB 61 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 120  
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGSLLMARAESDE 202  
DB 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGSLLMARAESDE 180  
QY 203 XYTMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 262  
DB 181 GTYMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 240  
QY 263 AVWLXWKVSGP 273  
DB 241 AVWLXWKVSGP 251

## RESULT 9

US-09-978-608A-211

; Sequence 211, Application US/09978608A

; Publication No. US20030045462A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC22

; CURRENT APPLICATION NUMBER: US/09/978,608A

; CURRENT FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 211

; LENGTH: 985

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-978-608A-211

Query Match 83.1%; Score 1337; DB 11; Length 985;  
Best Local Similarity 98.8%; Pred. No. 4.1e-101;  
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 23 MCGMAQDSPPQILVHPDQLFQGGPARMSCASQPPPTIRWLLNGQPLSNVPPDPHLL 82  
DB 1 MCGMAQDSPPQILVHPDQLFQGGPARMSCASQPPPTIRWLLNGQPLSNVPPDPHLL 60

QY 83 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 142  
DB 61 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDFOIQ 120  
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGSLLMARAESDE 202  
DB 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGSLLMARAESDE 180  
QY 203 XYTMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 262  
DB 181 GTYMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENTVLLNPDPAEGPKPRP 240  
QY 263 AVWLXWKVSGP 273  
DB 241 AVWLXWKVSGP 251

## RESULT 10

US-09-978-585A-211

; Sequence 211, Application US/09978585A

; Publication No. US20030049633A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

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; APPLICANT: Gerritsen, Mary E.

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; APPLICANT: Hillan, Kenneth J.

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; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC15

; CURRENT APPLICATION NUMBER: US/09/978,585A

; CURRENT FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 211

; LENGTH: 985

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-978-585A-211

Query Match 83.1%; Score 1337; DB 11; Length 985;  
Best Local Similarity 98.8%; Pred. No. 4.1e-101;  
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 23 MCGMAQDSPPQILVHPDQLFQGGPARMSCASQPPPTIRWLLNGQPLSNVPPDPHLL 82  
DB 1 MCGMAQDSPPQILVHPDQLFQGGPARMSCASQPPPTIRWLLNGQPLSNVPPDPHLL 60  
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; PRIOR APPLICATION NUMBER: 60/078936  
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 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337;; DB 11; Length 985;  
 Best Local Similarity 98.8%; Pred. No. 4.1e-101;  
 Matches: 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-04-29  
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;; PRIOR FILING DATE: 1998-05-15  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.1%; Score 1337; DB 10; Length 985;  
Best Local Similarity 98.8%; Pred. No. 4.1e-101;  
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 23 MCGMAQDSPPQILVHPDQLFGQPGFARMSCRSQPPPTIRWLNGQPLSNVPPDPHLL 82  
Db 1 MCGMAQDSPPQILVHPDQLFGQPGFARMSCOASQPPPTIRWLNGQPLSNVPPDPHLL 60  
QY 83 LPDGTLLILLLOPPARGHNDGQALSTDLGVYTCEASNRLGTAVSRGRLSVAVLREDFOIQ 142  
Db 61 LPDGTLLILLLOPPARGHNDGQALSTDLGVYTCEASNRLGTAVSRGRLSVAVLREDFOIQ 120  
QY 143 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHTVSGGSLLMARAEKSD 202

Db 121 PRDMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHTVSGGSLLMARAEKSD 180  
QY 203 XYTCVATNSAGHRESRAARVSIQEPQDYTFPEVLLAVRIQLENTVLNPDPAEGPKRPP 262  
Db 181 GTYTCVATNSAGHRESRAARVSIQEPQDYTFPEVLLAVRIQLENTVLNPDPAEGPKRPP 240  
QY 263 AVLWKVKVSGP 273  
Db 241 AVLWSKVSGP 251

## RESULT 8

US-09-978-189-211  
; Sequence 211, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
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; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR APPLICATION NUMBER: 60/077641  
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## RESULT 7

US-09-999-032A-211

; Sequence 211, Application US/09999832A

; Publication No. US20020192706A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
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; APPLICANT: Wood, William I.  
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; TITLE OF INVENTION: Acids Encoding the Same  
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RESULT 6  
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 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Deanoyers, Luc  
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 ; APPLICANT: Wood, William I.  
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APPLICANT: Godowski, Paul J.	PRIOR FILING DATE: 1998-03-31
APPLICANT: Grimaldi, J. Christopher	PRIOR APPLICATION NUMBER: 60/080194
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APPLICANT: Hillan, Kenneth J.	PRIOR APPLICATION NUMBER: 60/080327
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APPLICANT: Shelton, David L.	PRIOR FILING DATE: 1998-04-01
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/081070
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-04-08
APPLICANT: Williams, P. Mickey	PRIOR APPLICATION NUMBER: 60/081049
APPLICANT: Wood, William I.	PRIOR FILING DATE: 1998-04-08
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TITLE OF INVENTION: Acids Encoding the Same	PRIOR FILING DATE: 1998-04-08
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Db 121 PRDMVAVVGEQFTLECGPPMGHPEPTVSWKDGKPLALQPGRHVTSGSLLMAREAKSDE 180  
  
Qy 203 XYTMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENVTLLNPDPAEGPKRPP 262  
Db 181 GTYMCVATNSAGHRESRAARVSIQEPDYTEPVELLAVRIQLENVTLLNPDPAEGPKRPP 240  
  
Qy 263 AVWLXWKVSGP 273  
Db 241 AVWLXWKVSGP 251

RESULT 5  
US-09-978-697-211  
; Sequence 211, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter

;; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE  
;; FILE REFERENCE: 06501-098001  
;; CURRENT APPLICATION NUMBER: US/10/059,585  
;; CURRENT FILING DATE: 2002-01-29  
;; PRIOR APPLICATION NUMBER: PCT/JP00/05060  
;; PRIOR FILING DATE: 2000-07-28  
;; PRIOR APPLICATION NUMBER: US 60/183,322  
;; PRIOR FILING DATE: 2000-02-17  
;; PRIOR APPLICATION NUMBER: US 60/159,590  
;; PRIOR FILING DATE: 1999-10-18  
;; PRIOR APPLICATION NUMBER: JP 2000-118776  
;; PRIOR FILING DATE: 2000-01-11  
;; PRIOR APPLICATION NUMBER: JP 2000-183767  
;; PRIOR FILING DATE: 2000-05-02  
;; PRIOR APPLICATION NUMBER: JP 11-248036  
;; PRIOR FILING DATE: 1999-07-29  
;; NUMBER OF SEQ ID NOS: 64  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 22  
;; LENGTH: 792  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-059-585-22

Query Match 89.3%; Score 1436; DB 15; Length 792;  
Best Local Similarity 98.5%; Pred. No. 2.4e-109;  
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	MSGGDSLLGGGSLPLILLIMGMAGDSPPILVHPDQLFQGGPARMSCRAGSQPP	60
Db	1	MSGGDSLLGGGSLPLILLIMGMAGDSPPILVHPDQLFQGGPARMSCRAGSQPP	60
QY	61	PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTCEASNRL	120
Db	61	PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVYTCEASNRL	120
QY	121	GTAISRGARLSVAVLREDFQIQPRDMVAVGEGFTLEGCPWGHPEPTVSWKDKPLAL	180
Db	121	GTAISRGARLSVAVLREDFQIQPRDMVAVGEGFTLEGCPWGHPEPTVSWKDKPLAL	180
QY	181	QPRHTVSGGSLLMARAKSDKXTVMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV	240
Db	181	QPRHTVSGGSLLMARAKSDKXTVMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV	240
QY	241	RIQENVTLLNPDPAEGPKRPVAVLXWKVSGP	273
Db	241	RIQENVTLLNPDPAEGPKRPVAVLXWKVSGP	273

## RESULT 4

US-09-978-295A-211  
; Sequence 211, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James;  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630PIC11  
;; CURRENT APPLICATION NUMBER: US/09/978,295A  
;; CURRENT FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/064249  
;; PRIOR FILING DATE: 1997-11-03  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066364  
;; PRIOR FILING DATE: 1997-11-21  
;; PRIOR APPLICATION NUMBER: 60/077450  
;; PRIOR FILING DATE: 1998-03-10  
;; PRIOR APPLICATION NUMBER: 60/077632  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077641  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077791  
;; PRIOR FILING DATE: 1998-03-12  
;; PRIOR APPLICATION NUMBER: 60/078004  
;; PRIOR FILING DATE: 1998-03-13  
;; PRIOR APPLICATION NUMBER: 60/078886  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078936  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078910  
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;; PRIOR FILING DATE: 1998-03-27  
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;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/079728  
;; PRIOR FILING DATE: 1998-03-27  
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;; PRIOR FILING DATE: 1998-03-30  
;; PRIOR APPLICATION NUMBER: 60/079923  
;; PRIOR FILING DATE: 1998-03-30  
;; PRIOR APPLICATION NUMBER: 60/080105  
;; PRIOR FILING DATE: 1998-03-31  
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;; PRIOR FILING DATE: 1998-03-31  
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;; PRIOR APPLICATION NUMBER: 60/080194  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080327  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/080328  
;; PRIOR FILING DATE: 1998-04-01

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any amino acid
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86

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Best Local Similarity 100.0%; Pred. No. 1.8e-123;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGGDSLLGGGSLPLLLLLIMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPP 60
Db 1 MSGGDSLLGGGSLPLLLLLIMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPP 60

Qy 61 PTTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEASNRL 120
Db 61 PTTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEASNRL 120

Qy 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180
Db 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180

Qy 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
Db 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240

Qy 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXLPLNLTTPCSGPRLPREARELGRQR 300
Db 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXLPLNLTTPCSGPRLPREARELGRQR 300

Qy 301 NTG 303
Db 301 NTG 303

RESULT 2
US-10-411-224-86
; Sequence 86, Application US/10411224
; Publication No. US2003016906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22

; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (267)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (274)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (304)
; OTHER INFORMATION: Xaa equals stop translation
US-10-411-224-86

Query Match          99.6%; Score 1602; DB 12; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.8e-123;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGGDSLLGGGSLPLLLLLIMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPP 60
Db 1 MSGGDSLLGGGSLPLLLLLIMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPP 60

Qy 61 PTTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEASNRL 120
Db 61 PTTIRLLNGQPLSMVPPDPHLLPDGTLTLLQPPARGHAHQALSTDLGVYTCEASNRL 120

Qy 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180
Db 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180

Qy 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
Db 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240

Qy 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXLPLNLTTPCSGPRLPREARELGRQR 300
Db 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXLPLNLTTPCSGPRLPREARELGRQR 300

Qy 301 NTG 303
Db 301 NTG 303

RESULT 3
US-10-059-585-22
; Sequence 22, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayaashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Sencio, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

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(without alignments)  
2039.494 Million cell updates/sec

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Perfect score: 1608  
Sequence: 1 MGSGDSLGGKRSPLLL.....SGPRLPREARELGRQRTNG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

## Database : Published Applications AA:\*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	99.6	303	12 US-10-047-021-86	Sequence 86, Appl
2	1602	99.6	304	12 US-10-411-224-86	Sequence 86, Appl
3	1436	89.3	792	15 US-10-059-585-22	Sequence 22, Appl
4	1337	83.1	985	10 US-09-978-295A-211	Sequence 211, App
5	1337	83.1	985	10 US-09-978-697-211	Sequence 211, App
6	1337	83.1	985	10 US-09-978-192A-211	Sequence 211, App
7	1337	83.1	985	10 US-09-999-832A-211	Sequence 211, App
8	1337	83.1	985	11 US-09-978-189-211	Sequence 211, App
9	1337	83.1	985	11 US-09-978-608A-211	Sequence 211, App
10	1337	83.1	985	11 US-09-978-585A-211	Sequence 211, App
11	1337	83.1	985	11 US-09-978-191A-211	Sequence 211, App
12	1337	83.1	985	11 US-09-978-403A-211	Sequence 211, App
13	1337	83.1	985	11 US-09-978-564A-211	Sequence 211, App
14	1337	83.1	985	11 US-09-999-833A-211	Sequence 211, App
15	1337	83.1	985	11 US-09-981-915A-211	Sequence 211, App

16	1337	83.1	985	11	US-09-978-824-211	Sequence 211, App
17	1337	83.1	985	11	US-09-918-585A-211	Sequence 211, App
18	1337	83.1	985	11	US-09-978-423A-211	Sequence 211, App
19	1337	83.1	985	11	US-09-978-193A-211	Sequence 211, App
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25	1337	83.1	985	12	US-09-978-188A-211	Sequence 211, App
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27	1337	83.1	985	12	US-10-143-031A-211	Sequence 211, App
28	1337	83.1	985	12	US-10-002-967A-211	Sequence 211, App
29	1337	83.1	985	12	US-10-017-083A-211	Sequence 211, App
30	1337	83.1	985	12	US-10-143-030A-211	Sequence 211, App
31	1337	83.1	985	12	US-10-145-128A-211	Sequence 211, App
32	1337	83.1	985	12	US-10-017-191A-211	Sequence 211, App
33	1337	83.1	985	12	US-10-143-028A-211	Sequence 211, App
34	1337	83.1	985	12	US-10-143-029A-211	Sequence 211, App
35	1337	83.1	985	12	US-10-145-089A-211	Sequence 211, App
36	1337	83.1	985	12	US-10-013-926A-211	Sequence 211, App
37	1337	83.1	985	12	US-10-145-017A-211	Sequence 211, App
38	1337	83.1	985	12	US-10-164-728A-211	Sequence 211, App
39	1337	83.1	985	12	US-10-165-067A-211	Sequence 211, App
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41	1337	83.1	985	12	US-10-160-502A-211	Sequence 211, App
42	1337	83.1	985	12	US-10-165-247A-211	Sequence 211, App
43	1337	83.1	985	12	US-09-978-194A-211	Sequence 211, App
44	1337	83.1	985	12	US-09-978-681A-211	Sequence 211, App
45	1337	83.1	985	12	US-09-999-829A-211	Sequence 211, App

## ALIGNMENTS

RESULT 1  
US-10-047-021-86  
; Sequence 86, Application US/10047021  
; Publication No. US20040002591A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 50 Human Secreted Proteins  
; FILE REFERENCE: P2016P2  
; CURRENT APPLICATION NUMBER: US/10/047,021  
; CURRENT FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: US 60/262,066  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 09/722,329  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/262,109  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: PCT/US98/18360  
; PRIOR FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: US 60/057,626  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/057,663  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/057,669  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/058,667  
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; PRIOR APPLICATION NUMBER: US 60/058,973  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: US 60/058,666  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: US 60/090,112  
; PRIOR FILING DATE: 1998-06-22  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 303

SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-707-802-12

Query Match 14.4%; Score 232; DB 4; Length 607;  
Best Local Similarity 28.7%; Pred. No. 1.6e-14;  
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;

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QY	63	IRWLLNGQPLSMVPPDPHLLPDGTLTLLLPARGHAHDGOALSTDLGVYTCEASNRLGT	122
DB	71	YRWKMGTEMKLEPGSRHQLV-GGNLVIMNP-----TKAQDAGVYQCLASNPVGT	119
QY	123	AVSRGARLSVAVLREDFOIQPRDMV-AVVGQFTLECGPPMGHPPTVSWWKGKPLAL-	180
DB	120	VVSREAILRFGFLQE-FSKERDPYKAHEGWGVMPCNPPAHYFGLSYRWLLNEFPNFI	178
QY	181	QPGRHVS--GGSLIMARAESDXTVMCVATNSAGHRE-----SRAARVSIQ----	226
DB	179	TDGRHFVSQTTGNLYIARTNASDLGNYSCLATS---HMDFTKSVFSKFAQLNLAEDTR	235
QY	227	-----EPQDYTEPVVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLXW-KVSG	272
DB	236	LPAPSIKARFPAETVALVGQVTLCECFAGFNPVPR-----IKWRKVDG	278

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; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-716-679-3

Query Match      14.8%; Score 237.5; DB 2; Length 1501;
Best Local Similarity 30.9%; Pred. No. 1.6e-14;
Matches 72; Conservative 40; Mismatches 82; Indels 39; Gaps 11;

QY 13 GSLPLLLLLIMGMAQDPPQILVHPDQLFQGPGRMCRASQPPPTIRW-----LL 67
DB 14 GPVGLFLLVLLARGCLAEPPRIFRKPQDIGVGGVASFVQATGDPAPRTVWTKGKKV 73
QY 68 NGQPLSMVPPDPHLLPDGTLTLLLPARGHAHDGQALST--DLGVYTCASNRLGTAVS 125
DB 74 NSQRFETIDFDR-----SSGAVLRIQP-----LRTPRDENVYECVAQNSVG-EIT 117
QY 126 RGRALSVAVLREDFOIQPRDMVAVVGEQF-----TLGCGPPWHGHPPTVSWKDGK 176
DB 118 VHAKLT--VLRED-QLPFGFFNIDGPQKVVVTRTATMLCAAS-GNPDPEITWFKDFL 173
QY 177 PL--ALQPCR-HTVSGGSLMARAESDXTYMCVATNSAGHRESRAARVSQ 226
DB 174 VPDPSASNGRIKQLRSGALQIESSETDQGYECVATNSAGVRYSSPANLYVR 226

RESULT 14
US-08-752-307B-12
; Sequence 12, Application US/08752307B
; Patent No. 5952171
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752.307B
; FILING DATE: 19-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/020001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 607 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein

;
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-307B-12

Query Match      14.4%; Score 232; DB 2; Length 607;
Best Local Similarity 28.7%; Pred. No. 1.6e-14;
Matches 84; Conservative 41; Mismatches 108; Indels 60; Gaps 14;

QY 3 SGDSLILGSGSLPLLLLLLLIMGMAQDPPQILVHPDQLFQGPGRMCRASQPPPT 62
DB 23 SAMSALGSQTT-----FGPVFEDQPLSVL-FPEESTEE---QVLLACRARASPAT 70
QY 63 IRWLINGQPLSMVPPDPHLLPDGTLTLLLPARGHAHDGQALSTDLGVYTCASNRLGT 122
DB 71 YRWKONGTEMKLEFGSRHQLV-GGNLVIMNF-----TKAQDAGVYQCLASNPVGT 119
QY 123 AVSGARLSVAVLREDFOIQPRDMV-AVVGEOFTLECGPPWHGHPPTVSWKDGKPLAL- 180
DB 120 VVSREAILRFGLOE-FSKEERDPVKAHEGVMGLPCNPPAHYPGLSYRWLLNEFPNFI 178
QY 181 QPGRHTVS--GGSLLMARAESDXTYMCVATNSAGHRE-----SRAARVSQ----- 226
DB 179 TDGRHFVSQTTGNLYIARTNASDLGNYSCLATS---HMDFTKSVFSKFAQLNLAAEDTR 235
QY 227 -----BPQDYTEPVELLAVRIQLENTVTLNPDPAEGPKPRPAVWLXW-KVSG 272
DB 236 LFAPSIKARFPAETVALVGQQTLECFAGFNPVR-----IKWRKVDG 278

RESULT 15
US-09-707-802-12
; Sequence 12, Application US/09707802
; Patent No. 6391586
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/707.802
; FILING DATE: 07-No. 6391586-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/752.307
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/020001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 607 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,032
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN, JOHN W III
; REGISTRATION NUMBER: 35403
; REFERENCE/DOCKET NUMBER: 18992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-10166-5

Query Match 15.3%; Score 246; DB 5; Length 1911;
Best Local Similarity 30.9%; Pred. No. 3.2e-15;
Matches 75; Conservative 43; Mismatches 85; Indels 40; Gaps 11;

QY 2 GSGDLSLGRGSLPLLLLLIMGMAQDSPPQILVHPDQLFQGGPARMSCRASGQPP 61
DB 6 GPGMVSVGPMG---LLVLLVGGCAEPPRFPIKEPKDQIGVSGRVASFVCAQATGDKP 62
QY 62 TIRW-----LLNGQPLSMVPPDPHLLPDGTLILLLOPPARGHAHDGQALST--DLGVYTC 114
DB 63 RVTWNKKGKYSORFETIEFDE-----SAGAVLRIOQ-----LRTPRDENVYEC 107
QY 115 EASNRIGTAVSGKARLSVALRED-----FQIQPRDMVAVVGEQFTLECGPPWGHPE 166
DB 108 VAQNSVG-EITWAKLT--VLREDQLPSGFNIDMGFPOLKVERTRTATMLCAAS-GNPD 163
QY 167 PTVSMWKDGKPL--ALQPR- HTVSGGSLLMARAEKSDXTYMCVATNSAGHRSRAARV 223
DB 164 FEITWFKDFLPVDSASNGRIKQLRSGALQIESSEETDQGYECVATNSAGVRYSSPANTL 223
QY 224 SIQ 226
DB 224 YVR 226

RESULT 12
US-08-447-464-3
; Sequence 3, Application US/08447464
; Patent No. 5840842
; GENERAL INFORMATION:
; APPLICANT: Schlensing, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,464
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/130,570

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,032
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN, JOHN W III
; REGISTRATION NUMBER: 35403
; REFERENCE/DOCKET NUMBER: 18992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-10166-5

Query Match 14.8%; Score 237.5; DB 2; Length 1501;
Best Local Similarity 30.9%; Pred. No. 1.6e-14;
Matches 72; Conservative 40; Mismatches 82; Indels 39; Gaps 11;

QY 13 GSLPLLLLLLIMGMAQDSPPQILVHPDQLFQGGPARMSCRASGQPPPTIRW----LL 67
DB 14 GPGVGLVLLARGCLAEPPRFPIKEPKDQIGVSGRVASFVCAQATGDKPRTWNNKGV 73
QY 68 NGQPLSMVPPDPHLLPDGTLILLLOPPARGHAHDGQALST--DLGVYTCASNRLGTAVS 125
DB 74 NSQRFETIDFE-----SSGAVLRIOQ-----LRTPRDENVYECVAQNSVG-EIT 117
QY 126 RGARLSVALREDFQIQPRDMVAVVGEQF-----TLECGPPWGHPEPTVSMWKDGK 176
DB 118 VHAKLT--VLRED--QLPFGFNFIDMGFPOLKVERTRTATMLCAAS-GNPDPEITWFKDFL 173
QY 177 PL--ALQPR- HTVSGGSLLMARAEKSDXTYMCVATNSAGHRSRAARVSIQ 226
DB 174 PVDPSASNGRIKQLRSGALQIESSEETDQGYECVATNSAGVRYSSPANLYVR 226

RESULT 13
US-08-716-679-3
; Sequence 3, Application US/08716679
; Patent No. 5846800
; GENERAL INFORMATION:
; APPLICANT: Schlensing, Joseph
; APPLICANT: Yan, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,679
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/130,570
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
```



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,825A  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-800-825A-5

Query Match 15.3%; Score 246; DB 2; Length 1911;

Best Local Similarity 30.9%; Pred. No. 3.2e-15;

Matches 75; Conservative 43; Mismatches 85; Indels 40; Gaps 11;

QY 2 GSGDLSLLGGRSLPLLLLLMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPPP 61  
DB 6 GPGVSVVWPGM---LLVLLVGGCAAEPPRFKEPKDQIGVSGRVASFVCAATGDKPK 62  
QY 62 TIRW-----LLGQPLSMVPPPHLLPDGTLILLQPPARGHAHDGQALST--DLGVYTC 114  
DB 63 RVTWKKKKVNSQRFETIEFDE-----SAGAVLRQP-----LRTPRDENVYEC 107  
QY 115 EASNLGTAVSRGARLSVAVLRD-----FQIQPRDMVAVGGEQFTLEGCPWGHPE 166  
DB 108 VAQNSVG-EITVHAKLT--VLREDQLPSGFPNIDMGPKLVKVERTATMLCAAS-GNPD 163  
QY 167 PTVSWWKGKPL--ALQPR--HTVSGSLLMARAKSDEXTYMCVATNSAGHRESRAARV 223  
DB 164 PEITWFKDFLPVDPASNGRIKQLRSALQIESSEETDQGYECVATNSAGVRYSSPANL 223  
QY 224 SIQ 226  
DB 224 YVR 226

## RESULT 10

US-09-158-657-5  
Sequence 5, Application US/09158657  
Patent No. 6214564  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/158,657  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/800,825  
FILING DATE: 14-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-158-657-5

Query Match 15.3%; Score 246; DB 3; Length 1911;

Best Local Similarity 30.9%; Pred. No. 3.2e-15;

Matches 75; Conservative 43; Mismatches 85; Indels 40; Gaps 11;

QY 2 GSGDLSLLGGRSLPLLLLLMGMAQDSPQILVHPDQLFQGGPARMSCRASGQPPP 61  
DB 6 GPGVSVVWPGM---LLVLLVGGCAAEPPRFKEPKDQIGVSGRVASFVCAATGDKPK 62  
QY 62 TIRW-----LLGQPLSMVPPPHLLPDGTLILLQPPARGHAHDGQALST--DLGVYTC 114  
DB 63 RVTWKKKKVNSQRFETIEFDE-----SAGAVLRQP-----LRTPRDENVYEC 107  
QY 115 EASNLGTAVSRGARLSVAVLRD-----FQIQPRDMVAVGGEQFTLEGCPWGHPE 166  
DB 108 VAQNSVG-EITVHAKLT--VLREDQLPSGFPNIDMGPKLVKVERTATMLCAAS-GNPD 163  
QY 167 PTVSWWKGKPL--ALQPR--HTVSGSLLMARAKSDEXTYMCVATNSAGHRESRAARV 223  
DB 164 PEITWFKDFLPVDPASNGRIKQLRSALQIESSEETDQGYECVATNSAGVRYSSPANL 223  
QY 224 SIQ 226  
DB 224 YVR 226

## RESULT 11

PCT-US94-10166-5  
Sequence 5, Application PC/TUS9410166  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOHN W. WALLEN III  
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10166  
FILING DATE: 09-SEPT-1994  
CLASSIFICATION:



## RESULT 5

US-08-752-307B-14  
; Sequence 14, Application US/08752307B  
; Patent No. 5952171  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Gearing, David P.  
; APPLICANT: Levinson, Douglas A.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,307B  
; FILING DATE: 19-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 09404/020001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-752-307B-14

Query Match 15.6%; Score 251; DB 2; Length 630;  
Best Local Similarity 34.5%; Pred. No. 2.2e-16;  
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

QY 32 PQILVHPDQLFQPG-PARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILL 90  
DB 355 PYWLDEPQN-LILAPGEDGRILVCRANGPKPSIQWLNVGEPIEGSPNPSREVAGDTIVF 413  
QY 91 LQPPARGHAHDGOALSITDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPR----- 144  
DB 414 -----RDTQIGSS--AVYQCNASNEHGVL---ANAFSVUL-----DVPPRILAPRN 455  
QY 145 DMVAVVGQFT-LECGPPWGHPEPTVSWKDGKPLALQPGRHTV-SGGSLLMARAEKSD 202  
DB 456 QLIKVIQYNRTLDC-PFFGSPITLRFKNGQGNMLOGGNYKAHENGSLMSMARKEDQ 514  
QY 203 XYTMCVATNSAGHRESRAARVSIQEP 228  
DB 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

## RESULT 6

US-09-707-802-14  
; Sequence 14, Application US/09707802  
; Patent No. 6391586  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.

Gearing, David P.  
Levinson, Douglas A.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/707,802  
FILING DATE: 07-No. 6391586-2000  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/752,307  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 09404/020001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 630 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-707-802-14

Query Match 15.6%; Score 251; DB 4; Length 630;  
Best Local Similarity 34.5%; Pred. No. 2.2e-16;  
Matches 71; Conservative 34; Mismatches 71; Indels 30; Gaps 11;

QY 32 PQILVHPDQLFQPG-PARMSCRASGPPPTIRWLLNGQPLSMVPPDPHLLPDGTLILL 90  
DB 355 PYWLDEPQN-LILAPGEDGRILVCRANGPKPSIQWLNVGEPIEGSPNPSREVAGDTIVF 413  
QY 91 LQPPARGHAHDGOALSITDLGVYTCEASNRLGTAVSRGARLSVAVLRDFQIQPR----- 144  
DB 414 -----RDTQIGSS--AVYQCNASNEHGVL---ANAFSVUL-----DVPPRILAPRN 455  
QY 145 DMVAVVGQFT-LECGPPWGHPEPTVSWKDGKPLALQPGRHTV-SGGSLLMARAEKSD 202  
DB 456 QLIKVIQYNRTLDC-PFFGSPITLRFKNGQGNMLOGGNYKAHENGSLMSMARKEDQ 514  
QY 203 XYTMCVATNSAGHRESRAARVSIQEP 228  
DB 515 GIYTCVATNILGKVEAQ-VRLVKDP 539

## RESULT 7

US-09-991-326-14  
; Sequence 14, Application US/09991326  
; Patent No. 6395872  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; Gearing, David P.  
; Levinson, Douglas A.

TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES  
TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 14

```

; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1395
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-15

Query Match 25.2%; Score 405; DB 3; Length 1395;
Best Local Similarity 36.6%; Pred. No. 3.8e-31;
Matches 98; Conservative 38; Mismatches 104; Indels 28; Gaps 8;

Qy 15 LPLLLLLM---GGM---AODSPPOILVHPDQDLFOGPGPARMSCRASGQPPPTIRWLL 67
Db 32 LPAMLLLVASNLGPAVRGQYQSPRIETHTDLVKNQEPATLNCRVEGPEPTIEWFK 91

Qy 68 NQPLSMVPPDPHLL-LPDGTLILLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSR 126
Db 92 DGEPVSTNEKSHRVQPKDGLFFVYRTWQKKEQDG-----GEYVCVAKNRVQAVSR 144

Qy 127 GARLSVAVLREDFQIOPDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPL-----ALQP 182
Db 145 HASLQIAVLRRDFRVEPKDRTVAKGETALLCEGPPKGIPEPTLIWIKDGVFLDCLKAMSF 204

Qy 183 GRHT----VSGSLMARAESDXTYMCVATNSAGHRESRAARVSIQ-EPQDYTEPVEL 237
Db 205 GASSRVRVDGNNLLISNVEIDEGNYKICIAQLNLTGTRSSYAKLIVQKYPFKPKD- 263

Qy 238 LAVRIQLENVTLLNPDPAEGPKPPAVW 265
Db 264 ---QVLYGTATFCHSGVGGDPPPKVLW 288

RESULT 3
US-09-540-245A-17
; Sequence 17, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1297
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-245A-17

Query Match 22.2%; Score 356.5; DB 3; Length 1297;
Best Local Similarity 33.8%; Pred. No. 2.2e-26;

Matches 97; Conservative 45; Mismatches 104; Indels 41; Gaps 11;

Qy 27 AODSPPOILVHPDQDLFOGPGPARMSCRASGQPPPT---IRWLLNGQPL---SMVPPDPHLL 82
Db 25 ASNLAPVILIEHPIDVVVSRGSPATLNC---GAKPSTAKITWYKDGQPVITNKEQVNSHRI 81

Qy 83 LPD-GTLLLLQPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARLSVAVLREDFQI 141
Db 82 VLDTGSLFLLLKVNKGKNGKD-----SDAGAYVCASNEHGEVKSNEGSLKLAFLREDFRV 136

Qy 142 QPRDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPLALQP-GRHTV-SGSSLMARAESK 199
Db 137 RPRTVQALGEMAVLECSPPRGPEPVVSVWRKDKELRIQDMPRYTTLHSDGNLIIDPVDR 196

Qy 200 SDEXTYMCVATNSAGHRESRAARVSI-----QEPQDYTEPVELLAVRIQLENVTLLNP 252
Db 197 SDGTYQCVANNMVGERVSNPARLSVFEKPKFEQPKDMT-----VDVGAANVLDFC 247

Qy 253 DPAEGPKPPAVMLXWKVSGPXLPLNLTTRPCSGPRLPREARELRGQR 299
Db 248 RVTGDPQPOQ---ITWK-----RKNEPMPVTRAYIAKDNRLRIER 284

RESULT 4
US-09-540-245A-16
; Sequence 16, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1381
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-16

Query Match 21.5%; Score 345; DB 3; Length 1381;
Best Local Similarity 33.7%; Pred. No. 3.2e-25;
Matches 91; Conservative 31; Mismatches 102; Indels 46; Gaps 8;

Qy 32 PQILVHPDQDLFOGPGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLLPDTLLLL 91
Db 4 PRIIEHPMDTTPKNDPFTFNCAEQAGNPTPTIQFKDGRKLTDTGSHRIMLPAGGLFLL 63

Qy 92 QPPARGHAHDGQALSTDLGVYTCESNRLGTAVSRGARLSVAVLREDFQIOPDMVAVG 151
Db 64 KV-----IHSRR---ESDAGTYWCBAKNEFGVARSNATLQVAVLRDFRLEPANTRVAQG 116

Qy 152 EQFTLECGPPWGHPEPTVSWKDGKPLALQPR---HTVSGSLMARAESKSDXTYMCVA 209
Db 117 EVALMECGAPRGSPFQISWRKNGQTLNLVGNKRIRIVDGNLAIQEARQSDGDRYQCVV 176

Qy 210 TNSAGHRESRAARVS-----IOEPQDYTEPVELLAV---RIQLENVTLLNPDPAEGPK 259
Db 177 KVVVGTRESATAFLKVVHRPFLIRGPQNTAVGVSSVVFQCRI-----GGD 222

Qy 260 PRPAVMLXWKVSGPXLPLNLTTRPCSGPRLP 289
Db 223 PLPDV---LWR-----RTASGNMP 239
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:53:19 ; Search time 15.1762 Seconds  
(without alignments)  
844.758 Million.cell updates/sec

Title: US-10-047-021-86  
Perfect score: 1608  
Sequence: 1 MGSQDLSLGGKSLPLLLL.....SGPRLPRELRGQRRTG 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap: \*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap: \*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap: \*  
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5: /cgn2\_6/ptodata/1/iaa/6CTUS COMB.pap: \*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446.5	27.8	1651	3	US-09-540-245A-18
2	405	25.2	1295	3	US-09-540-245A-15
3	356.5	22.2	1297	3	US-09-540-245A-17
4	345	21.5	1381	3	US-09-540-245A-16
5	251	15.6	630	2	US-08-752-307B-14
6	251	15.6	630	4	US-09-707-802-14
7	251	15.6	630	4	US-09-991-326-14
8	246	15.3	1911	1	US-08-348-006B-5
9	246	15.3	1911	2	US-08-800-825A-5
10	246	15.3	1911	3	US-09-158-657-5
11	246	15.3	1911	5	PCT-US94-10166-5
12	237.5	14.8	1501	2	US-08-447-464-3
13	237.5	14.8	1501	2	US-08-716-679-3
14	232	14.4	607	2	US-08-752-307B-12
15	232	14.4	607	2	US-09-707-802-12
16	232	14.4	607	4	US-09-991-326-12
17	227.5	14.1	596	2	US-08-752-307B-13
18	227.5	14.1	596	4	US-09-707-802-13
19	227.5	14.1	596	4	US-09-991-326-13
20	206	12.8	1447	3	US-09-041-886-25
21	206	12.8	1447	5	PCT-US94-05277-2
22	203	12.6	615	2	US-08-752-307B-9
23	203	12.6	615	4	US-09-707-802-9
24	203	12.6	615	4	US-09-991-326-9
25	201.5	12.5	946	5	PCT-US95-08493-13
26	194.5	12.1	612	2	US-08-752-307B-11
27	194.5	12.1	612	4	US-09-707-802-11

28	194.5	12.1	612	4	US-09-991-326-11	Sequence 11, Appl
29	194.5	12.1	1268	4	US-08-506-296B-28	Sequence 28, Appl
30	193	12.0	1091	3	US-08-986-485-5	Sequence 5, Appl
31	193	12.0	1266	4	US-08-506-296B-4	Sequence 4, Appl
32	191	11.9	1260	4	US-08-506-296B-21	Sequence 21, Appl
33	188.5	11.7	1101	3	US-08-986-485-2	Sequence 2, Appl
34	186	11.6	416	4	US-09-638-649-1	Sequence 1, Appl
35	186	11.6	611	2	US-08-752-307B-10	Sequence 10, Appl
36	186	11.6	611	4	US-09-707-802-10	Sequence 10, Appl
37	186	11.6	611	4	US-09-991-326-10	Sequence 10, Appl
38	186	11.6	1253	4	US-08-506-296B-14	Sequence 14, Appl
39	180	11.2	1209	4	US-09-130-158A-2	Sequence 2, Appl
40	175.5	10.9	380	4	US-09-877-730-4	Sequence 4, Appl
41	175.5	10.9	904	4	US-09-877-730-6	Sequence 6, Appl
42	175.5	10.9	985	4	US-09-877-730-10	Sequence 10, Appl
43	175.5	10.9	1069	4	US-09-877-730-2	Sequence 2, Appl
44	175.5	10.9	1150	4	US-09-877-730-8	Sequence 8, Appl
45	175	10.9	462	2	US-08-752-307B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-09-540-245A-18  
; Sequence 18, Application US/09540245A  
; Patent No. 6270984  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey  
; APPLICANT: Kid, Thomas  
; APPLICANT: Brose, Katja  
; APPLICANT: Tessier-Lavigne, Marc  
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions  
; FILE REFERENCE: E98-031-3  
; CURRENT APPLICATION NUMBER: US/09/540,245A  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 60/065,544  
; PRIOR FILING DATE: 1997-11-14  
; PRIOR APPLICATION NUMBER: 60/081,057  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 1651  
; TYPE: PRT  
; ORGANISM: human  
; US-09-540-245A-18

Query Match	27.8%	Score 446.5;	DB 3;	Length 1651;
Best Local Similarity	41.7%	Pred. No. 3.7e-35;		
Matches	91;	Conservative 31;	Mismatches 87;	Indels 9; Gaps 2;
Qy	28	QDSPQILVHPQDLFGQPGPARMSCRASGPPPTIRWLNGQLPSLMVPPDPHH---	LLP 84	
Db	64	EDFPRIIVEHPSDLVKSGEPATLCKAEGRPPTIEWYKGERVETDKDDPRSHMLLP	123	
Qy	85	DGTLILLQPPARGHAHQALSTDLGYTCEASNRLGTAVSRGARLSVAVLRBDFQIOPR	144	
Db	124	SGSLFFLR-----IVHGRKSRPDEGVYCVARNYLGEAVSHNASLEVALLRDDFRQNP	177	
Qy	145	DMVAVVEQFTLECGPPWGHPEPTVSWKDGKPLALQGRHTVSGGSLLMARAEKSDEXT	204	
Db	178	DMVAVGEPAVMEQPPRGHPPEPTISWKDGSPDDDKDERTITRGKLMITYTRKSDAGK	237	
Qy	205	YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI	242	
Db	238	YVCVGTNMGRESEVAELTLVERPSFVKRPSNLAVTV	275	

RESULT 2  
US-09-540-245A-15  
; Sequence 15, Application US/09540245A  
; Patent No. 6270984

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Db	64	EDFPRIHVHPSDLIVSKGEPATLNCKAEGRETPTTIEWYKGERVETDKDDPRSHRMLLP	123
Qy	85	DGTLILLQPPARGHADGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLKREDFQIQPR	144
Db	124	SGSLFFLR-----IVHGRKSRPDEGVYCVARNYLGEAVSHNASLEVAILEDDEFRQNP	177
Qy	145	DMVAVVGEQFTLECGPPWGHPEPTVSWWKGKPLALQPGRHTVSGSLLMARAESDXT	204
Db	178	DVMVAVGEPVMECOPPRGHPEPTISWKKDGSFLDDKDERITIRGGKLMITVTRKSDAGK	237
Qy	205	YMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAVRI	242
Db	238	YVCVGTNMVGERESEVAELTVLERPSFVKRPSNLAVTV	275

Search completed: January 30, 2004, 15:54:42  
Job time : 40.2487 secs



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Db 139 DMVAVGEPVAVMEQPPRGHEPTISWKKDGPLDDKDERITIRGGKLMITYTRKSDAGK 198
Qy 205 YMCVATNSAGHRESRAARVSIOBPQDYTEPVELLAVRI 242
Db 199 YVCVTNMVGERSEVAELTVLERPSFVKRPSNLAVTV 236

RESULT 14
ABU04090
ID ABU04090 standard; Protein; 753 AA.
AC ABU04090;
XX
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #756.
XX
XX Translational profiling; expressed protein tag; EPT; kinase;
XX phosphatase; protease; protease inhibitor; transporter;
XX cytoskeletal protein; receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer;
XX gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX OS
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US09671.
XX
XX 28-MAR-2001; 2001US-279495P.
XX 21-MAY-2001; 2001US-292544P.
XX 08-AUG-2001; 2001US-310801P.
XX 01-OCT-2001; 2001US-326370P.
XX 04-DEC-2001; 2001US-336780P.
XX 20-FEB-2002; 2002US-358985P.
XX
XX (ZYCO-) ZYCOs INC.
XX
XX Chiciz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
XX or leukemia.
XX
XX Example 2; SEQ ID No 756; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor.
XX The polypeptide is useful as an immunogenic composition for eliciting
XX in a mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to
XX this polypeptide, is useful for treating cancer. The polypeptide is
XX also useful for identifying compounds that binds to a naturally
XX processed class I or class II MHC-binding polypeptide. The polypeptides
XX and polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling.
XX
XX Note: This sequence does not appear in the printed specification but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 753 AA;
```

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Query Match 27.8%; Score 446.5; DB 24; Length 753;
Best Local Similarity 41.7%; Pred. No. 2.3e-30;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 28 QDSPPQILVHPDQLFOGPGPARMSCRASQPPPTIRWLNGQPLSMVPPDPHH---LLP 84
Db 25 EDFPPRIVEHPSDLIIVSKGEPATLNCCKAEGRPTPTIEWYKGGERVETDKDPPSRHMLLP 84

Qy 85 DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLRDEFQIQPR 144
Db 85 SGSLFFLR-----IVHGRKSRPDEGVYCVARNYLGEAVSHNASLEVALRDDFRQNP 138

Qy 145 DMVAVGEOFTLECGPPGHPHPTVSWKDGKPLALQGRHTVSGGSLMARAEKSDXT 204
Db 139 DMVAVGEPVAVMEQPPRGHEPTISWKKDGPLDDKDERITIRGGKLMITYTRKSDAGK 198

Qy 205 YMCVATNSAGHRESRAARVSIOBPQDYTEPVELLAVRI 242
Db 199 YVCVTNMVGERSEVAELTVLERPSFVKRPSNLAVTV 236

RESULT 15
AY08404
ID AY08404 standard; Protein; 1649 AA.
AC AY08404;
XX
XX 24-JUL-1999 (first entry)
XX
XX Human ROBO1 protein.
XX
XX ROBO1; ROBO2; roundabout; nerve guidance; human; murine; cell function;
XX cell morphology; screening assay.
XX
XX Homo sapiens.
XX
XX WO9920764-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22164.
XX
XX 14-NOV-1997; 97US-0971172.
XX 20-OCT-1997; 97US-0062921.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Goodman CS, Kidd T, Mitchell KJ, Tear G;
XX
XX WPI; 1999-312615/26.
XX
XX N-PSDB; AAX08404.
XX
XX Robo polypeptides, a new immunoglobulin superfamily member
XX
XX Claim 1; Page 65-71; 80pp; English.
XX
XX This invention describes novel Robo (roundabout) polypeptides, involved
XX in nerve guidance which have been isolated from Drosophila sp.,
XX C. elegans, human and murine samples. The products of the invention can
XX be used to raise anti-Robo antibodies, which can be used to modulate cell
XX function or morphology. The Robo polynucleotides and fragments are useful
XX as probes and primers and for production of the Robo polypeptides. The
XX probes and primers are also useful in screening assays.
XX
XX Sequence 1649 AA;

Query Match 27.8%; Score 446.5; DB 20; Length 1649;
Best Local Similarity 41.7%; Pred. No. 6.3e-30;
Matches 91; Conservative 31; Mismatches 87; Indels 9; Gaps 2;

Qy 28 QDSPPQILVHPDQLFOGPGPARMSCRASQPPPTIRWLNGQPLSMVPPDPHH---LLP 84
Db 25 EDFPPRIVEHPSDLIIVSKGEPATLNCCKAEGRPTPTIEWYKGGERVETDKDPPSRHMLLP 84
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XX WPI; 2001-235372/24.  
DR N-PSDB; AAS01694.  
XX Isolated secreted proteins and their encoding nucleic acids are used  
PT for diagnosis and treatment of e.g. bacterial and viral infections,  
FT autoimmune diseases and inflammatory disorders -  
XX Claim 9; Fig 13; 261pp; English.  
XX The present sequence representing human TANGO 330 form 1 is  
CC isolated from cDNA clone jthA060922 from a human adrenal gland  
CC cDNA library. TANGO 330 is 1 of 4 novel human transmembrane proteins  
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)  
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins  
CC are useful as modulating agents in regulating a variety of cellular  
CC processes and can be used to express the proteins in a host cell in  
CC gene therapy applications. Antisense nucleic acid molecules and  
CC expression vectors containing the TANGO nucleic acids are also described.  
CC Diagnostic assays can be used to detect genetic alterations in the TANGO  
CC nucleic acids and to identify compounds that bind to or modulate activity  
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to  
CC monitor protein levels in tissue as a clinical testing procedure.  
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids  
CC and proteins may be used to diagnose, treat and monitor disorders of the  
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They  
CC can also be used to treat cell proliferative disorders (e.g. cancer),  
CC and neurological disorders e.g. Alzheimer's disease.  
XX Sequence 934 AA;  
SQ

Query Match 59.4%; Score 955; DB 22; Length 934;  
Best Local Similarity 98.9%; Pred. No. 9.4e-75;  
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 93 PPARGHAHDGQALSTDLGYVTCEASNRGLTAVSRGARLSVAVLRDFQIQPRDMVAVVGE 152  
DB 20 PPARGHAHDGQALSTDLGYVTCEASNRGLTAVSRGARLSVAVLRDFQIQPRDMVAVVGE 79  
QY 153 QFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGGSLLMARAEKSDXTYMCVATNS 212  
DB 80 QFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGGSLLMARAEKSDXTYMCVATNS 139  
QY 213 AGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLNPDPAEGPKPRPAVWLXWVSG 272  
DB 140 AGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLNPDPAEGPKPRPAVWLXWVSG 199  
QY 273 P 273  
DB 200 P 200

RESULT 13  
AAW83927  
ID AAW83927 standard; Protein; 753 AA.  
AC AAW83927;  
XX 01-MAR-1999 (first entry)  
DE Human T85 protein.  
XX T85; FMHB-6D4; FMHB-SD4; human; neurological disorder; therapy;  
KW diagnosis.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1..20 /label= sig\_peptide  
FT Peptide 21..753  
FT Protein /label= Mat\_protein  
FT 525..610  
FT Region

FT FT /note= "has homology to a fibronectin type III  
FT 638..727 domain"  
FT /note= "has homology to a fibronectin type III  
FT domain"  
FT 43..101  
FT /note= "has homology to a Ig superfamily domain"  
FT 145..203  
FT /note= "has homology to a Ig superfamily domain"  
FT 237..298  
FT /note= "has homology to a Ig superfamily domain"  
FT 329..394  
FT /note= "has homology to a Ig superfamily domain"  
FT 433..491  
FT /note= "has homology to a Ig superfamily domain"  
FT 247..249  
FT /note= "RGD motif"  
FT 516..600  
FT /note= "cytokine receptor homology N-terminal  
FT domain"  
XX WO9848051-A2.  
XX 29-OCT-1998.  
XX 17-APR-1998; 98WO-US07714.  
XX 10-OCT-1997; 97US-0062017.  
XX 18-APR-1997; 97US-0044746.  
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
XX Holtzman D, McCarthy SA;  
XX WPI; 1999-024021/02.  
XX N-PSDB; AAV69278.  
XX New isolated human FTHMA-070 and T85 proteins - used to develop  
XX products for the diagnosis and therapy of disorders involving  
XX cellular processes, e.g. neuronal development.  
XX Claim 31; Fig 3; 127pp; English.  
XX This is the amino acid sequence of a novel human protein designated  
XX T85, and also referred to as FMHB-6D4 and FMHB-SD4. T85 cDNA (see  
XX AAV69278) was identified in a human fetal brain cDNA library using a  
XX screen designed to identify genes encoding proteins having a  
XX functional signal sequence. T85 nucleic acids and polypeptides of  
XX the invention are useful as modulating agents in regulating a  
XX variety of cellular processes. They can be used for identifying  
XX compounds which bind to or modulate the activity of the polypeptides  
XX (claimed). They can also be used in screening assays, detection  
XX assays (e.g. chromosomal mapping, tissue typing, forensic biology),  
XX predictive medicine (e.g. diagnostic assays, prognostic assays,  
XX monitoring clinical trials, and pharmacogenomics), and methods of  
XX treatment (e.g. therapeutic and prophylactic) e.g. for neurological  
XX disorders.  
XX Sequence 753 AA;  
SQ

Query Match 27.8%; Score 446.5; DB 20; Length 753;  
Best Local Similarity 41.7%; Pred. No. 2.3e-30;  
Matches 91; Conservative 31; Mismatches 8; Indels 9; Gaps 2;  
QY 28 QDSPPQLVHPDQDLFOGPGFARMSCRASGPPPTIRWLLNGQLPSVMVPPPHH---LLP 84  
DB 25 EDFPPRIVEHPSDLIVSGKEPATLNCRAEGRPTTIEWYKGERVETDKDPPSRHMLLP 84  
QY 85 DGTLLLOPPARGHAHDGQALSTDLGYVTCEASNRGLTAVSRGARLSVAVLRDFQIQPR 144  
DB 85 SGLFLFLR-----IVHGRKSRPDEGVVVCARNYLGEAVSHNASLEVAILLRDDPQNS 138  
QY 145 DMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGHRTVSGGSLLMARAEKSDXT 204

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AC AAU00500;
XX 18-JUL-2001 (first entry)
XX
XX Human TANGO 330 form 1 protein.
XX
XX Human; TANGO 315; clone jthaa060g22; TANGO 330; TANGO 437; TANGO 480;
KW cellular process regulator; gene therapy; adrenal gland; cancer;
KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..393
XX /label= Extracellular_domain
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XX Misc-difference 1 /note= "Alternatively this residue is Asp due to
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XX Misc-difference 2 /note= "Alternatively this residue is Ser due to
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XX Misc-difference 3 /note= "Alternatively this residue is Val due to
XX species variation"
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XX Modified-site 29..34 /note= "N-myristylation site"
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XX Modified-site 37..42 /note= "N-myristylation site"
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XX Modified-site 44..46 /note= "Protein kinase C phosphorylation site"
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XX Modified-site 48..53 /note= "N-myristylation site"
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XX Misc-difference 53 /note= "Alternatively this residue is Lys due to
XX species variation"
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XX Modified-site 54..59 /note= "N-myristylation site"
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XX Domain 78..136
XX /label= Ig-like_domain
XX
XX Modified-site 126..132 /note= "Tyrosine kinase phosphorylation site"
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XX Modified-site 130..135 /note= "N-myristylation site"
XX
XX Modified-site 151..154 /note= "Casein kinase II phosphorylation site"
XX
XX Modified-site 173..176 /note= "Asn is N-glycosylated"
XX
XX Modified-site 194..196 /note= "Protein kinase C phosphorylation site"
XX
XX Modified-site 221..226 /note= "N-myristylation site"
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XX Modified-site 239..244 /note= "N-myristylation site"
XX
XX Modified-site 254..256 /note= "N-myristylation site"
XX
XX Modified-site 282..284 /note= "Protein kinase C phosphorylation site"
XX
XX Modified-site 287..290 /note= "Protein kinase C phosphorylation site"
XX
XX Modified-site 304..309 /note= "Asn is N-glycosylated"
XX
XX Modified-site 316..319 /note= "N-myristylation site"
XX
XX Modified-site 323..326 /note= "Asn is N-glycosylated"
XX
XX Modified-site 331..334 /note= "Asn is N-glycosylated"
XX
XX Modified-site 352..357 /note= "Casein kinase II phosphorylation site"
XX
XX Modified-site 391..393 /note= "N-myristylation site"
XX
XX Modified-site 394..417 /note= "Protein kinase C phosphorylation site"
XX
XX Domain

FT /label= Transmembrane_domain
FT 411..416 /note= "N-myristylation site"
FT
FT 418..934 /label= Cytoplasmic_domain
FT
FT Modified-site
FT 434..437 /note= "Casein kinase II phosphorylation site"
FT
FT Modified-site
FT 455..457 /note= "Protein kinase C phosphorylation site"
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FT Modified-site
FT 472..474 /note= "Protein kinase C phosphorylation site"
FT
FT Modified-site
FT 510..515 /note= "N-myristylation site"
FT
FT Modified-site
FT 546..559 /note= "Casein kinase II phosphorylation site"
FT
FT Modified-site
FT 553..555 /note= "Protein kinase C phosphorylation site"
FT
FT Modified-site
FT 559..561 /note= "Protein kinase C phosphorylation site"
FT
FT Modified-site
FT 601..606 /note= "N-myristylation site"
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FT 607..610 /note= "Asn is N-glycosylated"
FT
FT Modified-site
FT 632..635 /note= "Casein kinase II phosphorylation site"
FT
FT Modified-site
FT 701..703 /note= "Protein kinase C phosphorylation site"
FT
FT Modified-site
FT 711..714 /note= "Casein kinase II phosphorylation site"
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FT 721..724 /note= "Casein kinase II phosphorylation site"
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FT Modified-site
FT 732..735 /note= "Casein kinase II phosphorylation site"
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FT 737..739 /note= "Protein kinase C phosphorylation site"
FT
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FT 762..765 /note= "Casein kinase II phosphorylation site"
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FT 794..797 /note= "Casein kinase II phosphorylation site"
FT
FT Modified-site
FT 798..803 /note= "N-myristylation site"
FT
FT Modified-site
FT 806..809 /note= "Casein kinase II phosphorylation site"
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FT 814..816 /note= "Protein kinase C phosphorylation site"
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FT 821..824 /note= "Casein kinase II phosphorylation site"
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FT Modified-site
FT 825..830 /note= "N-myristylation site"
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FT 865..867 /note= "Protein kinase C phosphorylation site"
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FT 865..868 /note= "Casein kinase II phosphorylation site"
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FT Modified-site
FT 875..878 /note= "Asn is N-glycosylated"
FT
FT Modified-site
FT 896..898 /note= "Protein kinase C phosphorylation site"
FT
FT Modified-site
FT 914..916 /note= "Protein kinase C phosphorylation site"
FT
FT Modified-site
FT 929..932 /note= "Casein kinase II phosphorylation site"
FT
FT
XX WO200123523-A2.
XX
XX 05-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US27202.
XX
XX 30-SEP-1999; 99US-0409634.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kirst S, Wrighton N, Fraser CC;
```

XX WPI; 2001-235372/24.  
DR N-PSDB; AAS01695.  
XX  
XX Isolated secreted proteins and their encoding nucleic acids are used  
PT for diagnosis and treatment of e.g. bacterial and viral infections,  
PT autoimmune diseases and inflammatory disorders -  
XX  
XX Claim 9; Fig 14; 261pp; English.  
XX  
XX The present sequence representing human TANGO 330 form 2 is  
CC isolated from cDNA Clone Jthx181e12 from a human astrocyte cDNA  
CC library. TANGO 330 is 1 of 4 novel human transmembrane proteins  
CC which also includes TANGO 315 (AAU00498-AAU00499), TANGO 437 (AAU00502)  
CC and TANGO 480 (AAU00503). The nucleic acids encoding these proteins  
CC are useful as modulating agents in regulating a variety of cellular  
CC processes and can be used to express the proteins in a host cell in  
CC gene therapy applications. Antisense nucleic acid molecules and  
CC expression vectors containing the TANGO nucleic acids are also described.  
CC Diagnostic assays can be used to detect genetic alterations in the TANGO  
CC nucleic acids and to identify compounds that bind to or modulate activity  
CC of the TANGO proteins. Anti-TANGO antibodies are used diagnostically to  
CC monitor protein levels in tissue as a clinical testing procedure.  
CC TANGO 330 shows homology to human Roundabout. TANGO 330 nucleic acids  
CC and proteins may be used to diagnose, treat and monitor disorders of the  
CC adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and neoplasia. They  
CC can also be used to treat cell proliferative disorders (e.g. cancer),  
CC and neurological disorders e.g. Alzheimer's disease.  
XX  
XX Sequence 480 AA;  
Query Match 82.8%; Score 1332; DB 22; Length 480;  
Best Local Similarity 98.8%; Pred.No. 4.1e-108;  
Matches 247; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 24 GCGAQQSPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLL 83  
DB 55 GCGAQQSPQILVHPQDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSMVPPDPHLL 114  
QY 84 PDGTLILLOPPARGHAHQALSTDLGVYTCASNRLGTAVSARGARLSVAVLREDFOIQP 143  
DB 115 PDGTLILLOPPARGHAHQALSTDLGVYTCASNRLGTAVSARGARLSVAVLREDFOIQP 174  
QY 144 RDMVAVGQFTLECGPPMGHPPTVSWKDGKPLALQPGRTVSGSLLMARAEKSDX 203  
DB 175 RDMVAVGQFTLECGPPMGHPPTVSWKDGKPLALQPGRTVSGSLLMARAEKSDX 234  
QY 204 TYMCVATNSAGHRESRAARVSIQEPQDYTEPVVLLAVRIQLENVTLNPDPAEGPKRPA 263  
DB 235 TYMCVATNSAGHRESRAARVSIQEPQDYTEPVVLLAVRIQLENVTLNPDPAEGPKRPA 294  
QY 264 VMLXWKVSGP 273  
DB 295 VMLXWKVSGP 304  
RESULT 11  
AAU99420  
ID AAU99420 standard; Protein; 1015 AA.  
XX  
XX AAU99420;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Mouse ECSM4 protein #1.  
XX  
XX Mouse; endothelial cell-specific molecule 4; ECSM4; neovasculture;  
KW imaging vascular endothelium; proliferative disease; cancer;  
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;  
KW endothelial damage; tumour neovasculture; cardiac disease;  
KW endometriosis; hypoxic condition; angiogenesis; cytosstatic;  
KW cardiant.

OS Mus sp.  
XX WO200236771-A2.  
XX  
XX 10-MAY-2002.  
XX  
XX 06-NOV-2001; 2001WO-GB04906.  
XX  
XX 06-NOV-2000; 2000US-245566P.  
XX 07-MAR-2001; 2001US-273662P.  
XX  
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
XX Bicknell R, Huminteki L;  
XX WPI; 2002-508120/54.  
XX N-PSDB; ABK87138.  
XX  
XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for  
PT imaging, diagnosing and treating a condition involving vascular  
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -  
XX  
XX Disclosure; Fig 13; 248pp; English.  
XX  
XX The present invention relates to endothelial cell-specific molecule 4  
XX (ECSM4), and the polynucleotide sequences encoding it. The ECSM4  
XX proteins are useful for imaging vascular endothelium in the body of  
XX an individual, and for diagnosing and treating a proliferative  
XX disease or condition involving the vascular endothelium (preferably,  
XX neovasculture) such as cancer, psoriasis, diabetic retinopathy,  
XX atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in  
XX the manufacture of diagnostic or prognostic agent for such conditions.  
XX The proteins are also useful for detecting endothelial damage or  
XX activation, detecting a tumour or tumour neovasculture, cardiac  
XX disease, or endometriosis by detecting the amount of ECSM4 present in  
XX a sample. The polynucleotide sequences encoding ECSM4 are useful in  
XX gene therapy for treating a hypoxic condition such as cancer, cardiac  
XX disease, endometriosis or atherosclerosis and in the manufacture of  
XX medicaments for treating the above disease. The sequences are useful  
XX for modulating angiogenesis in an individual. The present sequence  
XX represents a mouse ECSM4 protein.  
SQ Sequence 1015 AA;  
Query Match 69.2%; Score 1112.5; DB 23; Length 1015;  
Best Local Similarity 77.4%; Pred.No. 1.7e-88;  
Matches 212; Conservative 20; Mismatches 41; Indels 1; Gaps 1;  
QY 1 MGSGGDSILGGRGSLPLLLLLIMGMAQDSPPQILVHPQDQLFQGGPARMSCRASGQPP 60  
DB 11 MGSGGTGLGTWEPPLPLLLFIMGGEALDSPQILVHPQDQLFQGGPARMSCRASGQPP 70  
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLOPPARGHAHQALSTDLGVYTCASN 119  
DB 71 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLOPPARGHAHQALSTDLGVYTCASN 130  
QY 120 LGTAVSRGARLSVAVLREDFOIQPRDVMVAVGQFTLECGPPMGHPPTVSWKDGKPLA 179  
DB 131 LGTAVSRGARLSVAVLREDFOIQPRDVMVAVGQFTLECGPPMGHPPTVSWKDGKPLV 190  
QY 180 LQGRHTVSGSLLMARAEKSDXTCVATNSAGHRESRAARVSIQEPQDYTEPVVLLA 239  
DB 191 LQGRHTVSGSLLMARAEKSDXTCVATNSAGHRESRAARVSIQEPQDYTEPVVLLA 250  
QY 240 VRIQLENVTLNPDPAEGPKRPAVAVLXWKVSGP 273  
DB 251 VRIQLENVTLNPDPAEGPKRPAVAVLXWKVSGP 284  
RESULT 12  
AAU00500  
ID AAU00500 standard; Protein; 934 AA.  
XX

PT encoding them useful for treating cancer, kidney diseases, bone,  
 PT cartilage disorders and immune deficiencies -  
 XX Claim 12; Fig 77; 459pp; English.  
 PS  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists. The  
 CC bioactive molecule may be a toxin, radiolabel or antibody, and causes  
 CC apoptosis or death of the cell. The PRO polypeptides are useful for  
 CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,  
 CC cardiac insufficiency, nervous system disorders, kidney disorders,  
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.  
 CC The polynucleotide sequences encoding PRO polypeptides are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
 CC generating transgenic animals or knockout animals, for the genetic  
 CC analysis of individuals with genetic disorders, and in gene therapy.  
 CC ABU61071-ABU61164 represent the human PRO polypeptides of the  
 CC invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdsIDentry.html.  
 XX  
 SQ Sequence 985 AA;

Query Match 83.1%; Score 1337; DB 24; Length 985;  
 Best Local Similarity 98.8%; Pred. No. 3.7e-108;  
 Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 23 MGGMAQDSPPQLLVHPDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSWPPDPHLL 82  
 Db 1 MGGMAQDSPPQLLVHPDQLFQGGPARMSCRASGQPPPTIRWLLNGQPLSWPPDPHLL 60  
 QY 83 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCASNRLGTAVSGARLSVAVLRDFQIQ 142  
 Db 61 LPDGTLLLLQPPARGHAGDQALSTDLGVYTCASNRLGTAVSGARLSVAVLRDFQIQ 120  
 QY 143 PRDWAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQGRHTVSGSLMARAEKSD 202  
 Db 121 PRDWAVVGEQFTLECGPPWGHPEPTVSWKDGKPLALQGRHTVSGSLMARAEKSD 180  
 QY 203 XYTMCVATNSAGHRESRAARVSIQSPDYTERVELLAVRIQLENTVLLNPDPAEGPKRPP 262  
 Db 181 GTYMCVATNSAGHRESRAARVSIQSPDYTERVELLAVRIQLENTVLLNPDPAEGPKRPP 240  
 QY 263 AVWLXWKVSGP 273  
 Db 241 AVWLXWKVSGP 251

RESULT 10  
 AAU00501  
 ID AAU00501 standard; Protein; 480 AA.  
 XX  
 AC AAU00501;  
 XX

DT 18-JUL-2001 (first entry)

DE Human TANGO 330 form 2 protein.

XX Human; TANGO 315; clone Jthx181e12; TANGO 330; TANGO 437; TANGO 480;  
 KW cellular process regulator; gene therapy; astrocyte; cancer;  
 KW Roundabout; adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;  
 KW cell proliferative disorder; neurological disorder; Alzheimer's disease.

OS Homo sapiens.

XX Key Location/Qualifiers

PI Kirst S, Wrighton N, Fraser CC;

FT Peptide  
 FT 1..20 /label= Signal\_peptide  
 FT Modified-site  
 FT 15..17 /note= "Protein kinase C phosphorylation site"  
 FT Domain  
 FT 21..480 /label= Extracellular\_domain  
 FT Protein  
 FT 21..480 /label= Mature\_TANGO\_330\_form\_2\_protein  
 FT Modified-site  
 FT 30..33 /note= "cAMP and cGMP dependent protein kinase phosphorylation site"  
 FT Modified-site  
 FT 44..47 /note= "Casein kinase II phosphorylation site"  
 FT Domain  
 FT 77..147 /label= Ig-like\_domain  
 FT Modified-site  
 FT 93..95 /note= "Protein kinase C phosphorylation site"  
 FT Modified-site  
 FT 100..105 /note= "N-myristylation site"  
 FT Modified-site  
 FT 133..138 /note= "N-myristylation site"  
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 FT 141..146 /note= "N-myristylation site"  
 FT Modified-site  
 FT 148..150 /note= "N-myristylation site"  
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 FT Modified-site  
 FT 158..163 /note= "N-myristylation site"  
 FT Domain  
 FT 182..240 /label= Ig-like\_domain  
 FT Modified-site  
 FT 230..236 /note= "Tyrosine kinase phosphorylation site"  
 FT Modified-site  
 FT 234..239 /note= "N-myristylation site"  
 FT Modified-site  
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 FT Modified-site  
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 FT Modified-site  
 FT 325..330 /note= "N-myristylation site"  
 FT Modified-site  
 FT 343..348 /note= "N-myristylation site"  
 FT Modified-site  
 FT 358..360 /note= "Protein kinase C phosphorylation site"  
 FT Modified-site  
 FT 386..388 /note= "Protein kinase C phosphorylation site"  
 FT Modified-site  
 FT 391..394 /note= "Asn is N-glycosylated"  
 FT Modified-site  
 FT 408..413 /note= "N-myristylation site"  
 FT Modified-site  
 FT 420..423 /note= "Asn is N-glycosylated"  
 FT Modified-site  
 FT 427..430 /note= "Asn is N-glycosylated"  
 FT Modified-site  
 FT 435..438 /note= "Casein kinase II phosphorylation site"  
 FT Modified-site  
 FT 456..461 /note= "N-myristylation site"

WO200123523-A2.

05-APR-2001.

02-OCT-2000; 2000WO-US27202.

30-SEP-1999; 99US-0409634.

(MILL-) MILLENNIUM PHARM INC.

Db 1 MCGMAQDSPPQILVHPQDLQFGPGPARMSCASQPPETIRWLLNGQPLSMVPPDPHLL 60  
QY 83 LPDGTLLILQPPARGHAHQALSTDLGVYTCEASNRLCTAVSARGARLSVAVLREDFOIQ 142  
Db 61 LPDGTLLILQPPARGHAHQALSTDLGVYTCEASNRLCTAVSARGARLSVAVLREDFOIQ 120  
QY 143 PRDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHVTSGGSLLMARAEKSD 202  
Db 121 PRDMVAVGEQFTLECGPPWGHPEPTVSWKDGKPLALQPGRHVTSGGSLLMARAEKSD 180  
QY 203 XYTMCVATNSAGHRSRAARVSIQBPQDYTPVELLAVRIQLENTVLLNPDPAEGPKRPP 262  
Db 181 GTYMCVATNSAGHRSRAARVSIQBPQDYTPVELLAVRIQLENTVLLNPDPAEGPKRPP 240  
QY 263 AVLXWKVSGP 273  
Db 241 AVLXWKVSGP 251  
  
RESULT 9  
ABU61102  
ID ABU61102 standard; Protein; 985 AA.  
XX  
AC ABU61102;  
XX  
DT 08-MAY-2003 (first entry)  
XX  
DE Human PRO860 polypeptide.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
KW cardiac insufficiency; nervous system disorder; kidney disorder;  
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;  
KW genetic disorder; cystostatic; antidiabetic; antiinflammatory;  
KW antarthritic; anti-tumour; vulnerary; antianaemic; dermatological;  
KW cardiant.  
XX  
OS Homo sapiens.  
XX  
PN US2002169284-A1.  
XX  
PD 14-NOV-2002.  
XX  
PF 16-OCT-2001; 2001US-0978697.  
XX  
PR 07-OCT-1998; 98WO-US21141.  
PR 20-NOV-1998; 98WO-US24855.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.

PR 24-AUG-2000; 2000WO-US23328.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 22-MAR-2001; 2001WO-US09552.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 17-OCT-1997; 97US-062250P.  
PR 03-NOV-1997; 97US-064249P.  
PR 13-NOV-1997; 97US-065311P.  
PR 21-NOV-1997; 97US-066364P.  
PR 10-MAR-1998; 98US-077450P.  
PR 11-MAR-1998; 98US-077632P.  
PR 11-MAR-1998; 98US-077641P.  
PR 11-MAR-1998; 98US-077649P.  
PR 12-MAR-1998; 98US-077791P.  
PR 13-MAR-1998; 98US-078004P.  
PR 20-MAR-1998; 98US-078886P.  
PR 20-MAR-1998; 98US-078910P.  
PR 20-MAR-1998; 98US-078936P.  
PR 20-MAR-1998; 98US-078939P.  
PR 25-MAR-1998; 98US-079294P.  
PR 26-MAR-1998; 98US-079656P.  
PR 27-MAR-1998; 98US-079663P.  
PR 27-MAR-1998; 98US-079664P.  
PR 27-MAR-1998; 98US-079689P.  
PR 27-MAR-1998; 98US-079728P.  
PR 27-MAR-1998; 98US-079786P.  
PR 30-MAR-1998; 98US-079920P.  
PR 30-MAR-1998; 98US-079923P.  
PR 26-MAY-1981; 81US-0267213.  
PR 17-MAR-1998; 98US-0040220.  
PR 26-JUN-1998; 98US-0105413.  
PR 02-OCT-1998; 98US-0168978.  
PR 02-NOV-1998; 98US-0184216.  
PR 06-NOV-1998; 98US-0187368.  
PR 07-DEC-1998; 98US-0202054.  
PR 22-DEC-1998; 98US-0218517.  
PR 05-MAR-1999; 99US-0254465.  
PR 10-MAR-1999; 99US-0265686.  
PR 12-APR-1999; 99US-0284291.  
PR 14-MAY-1999; 99US-0311832.  
PR 14-MAY-1999; 99US-0380137.  
PR 25-AUG-1999; 99US-0380138.  
PR 25-AUG-1999; 99US-0380142.  
PR 08-NOV-2000; 2000US-0709238.  
PR 27-NOV-2000; 2000US-0723749.  
PR 20-DEC-2000; 2000US-0747259.  
PR 22-MAR-2001; 2001US-0816744.  
PR 22-MAR-2001; 2001US-0816920.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 30-JUL-2001; 2001US-0918585.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
XX  
XX WPI; 2003-288163/28.  
DR N-PSDB; AEX92441.  
XX  
PT Novel secreted and transmembrane polypeptides and polynucleotides





```
XX (HELI-) HELIX RES INST.
XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX WPI; 2001-564736/63.
DR N-PSDB; AAH78073.
XX
PT New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes -
XX
XX Claim 2; Page 175-180; 336pp; Japanese.
XX
CC The present sequence represents a human protein kinase/protein
CC phosphatase. The polypeptides are expected to participate in signal
CC transduction in cells. The kinase phosphatases are connected with
CC intracellular signalling pathways. Antisense oligonucleotides and
CC compounds identified by screening (agonists or antagonists) can be
CC used to treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules for drug development.
XX
SQ Sequence 792 AA;
Query Match 89.3%; Score 1436; DB 22; Length 792;
Best Local Similarity 98.5%; Pred. No. 66-117;
Matches 269; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPQDQLFQGGPARMSCRASGQPP 60
Db 1 MSGGDSLLGGRGSLPLLLLLIMGMAQDSPPQILVHPQDQLFQGGPARMSCRASGQPP 60
QY 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVVTCASNRL 120
Db 61 PTIRWLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAHDGQALSTDLGVVTCASNRL 120
QY 121 GTAVSRGARLSVAVLRDFQIOPRDMVAVGGEFTLECGPPMGHPPTVSWMKDKPLAL 180
Db 121 GTAVSRGARLSVAVLRDFQIOPRDMVAVGGEFTLECGPPMGHPPTVSWMKDKPLAL 180
QY 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDTEPVELLAV 240
Db 181 QPGRHTVSGGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDTEPVELLAV 240
QY 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGP 273
Db 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGP 273
RESULT 7
AA41716
ID AA41716 standard; Protein; 985 AA.
XX
AC AA41716;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO860 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-050528.
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XX 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 30-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 07-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 13-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
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QY 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
QY 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXRLLPNLTRPCSGPRLPREARELKGRR 300
DB 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGPXRLLPNLTRPCSGPRLPREARELKGRR 300
QY 301 NTG 303
DB 301 NTG 303

RESULT 3
ID ABB97310 standard; Protein; 1007 AA.
XX
AC ABB97310;
DT 27-JUN-2002 (first entry)
DE Novel human protein SEQ ID NO: 578.
XX
KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US26015.
XX
PR 11-SEP-2000; 2000US-0659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR N-PSDB; ABN32496.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis -
XX
PS Example 2; SEQ ID NO 578; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibit e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention.
XX
SQ Sequence 1007 AA;
Query Match 89.8%; Score 1444; DB 23; Length 1007;
Best Local Similarity 98.9%; Pred. No. 1.6e-117;
Matches 270; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGSQDSSLQGRGSLPLLLLLIMGMAQDSPQILVHPQDLFCGPGPARMSCRAGQPP 60
DB 1 MGSQDSSLQGRGSLPLLLLLIMGMAQDSPQILVHPQDLFCGPGPARMSCRAGQPP 60
```

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QY 61 PTIRLLNGQFLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGYVTCESNRL 120
DB 61 PTIRLLNGQFLSMVPPDPHLLPDGTLTLLQPPARGHAHDGQALSTDLGYVTCESNRL 120
QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
DB 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
QY 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAEKSDXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
QY 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGP 273
DB 241 RIQLENTVLLNPDPAEGPKPRPAVWLXWKVSGP 273

RESULT 4
ID AAU99419 standard; Protein; 1104 AA.
XX
AC AAU99419;
DT 07-OCT-2002 (first entry)
DE Human ECSM4 protein.
XX
KW Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW imaging vascular endothelium; proliferative disease; cancer;
KW psoriasis; diabetic retinopathy; atherosclerosis; menorrhagia;
KW endothelial damage; tumour neovasculature; cardiac disease;
KW endometriosis; hypoxic condition; angiogenesis; cytostatic;
KW cardiant.
XX
OS Homo sapiens.
XX
PN WO200236771-A2.
XX
PD 10-MAY-2002.
XX
PF 06-NOV-2001; 2001WO-GB04906.
XX
PR 06-NOV-2000; 2000US-245566P.
XX
PR 07-MAR-2001; 2001US-273662P.
XX
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
PI Bicknell R, Huminiecki L;
XX
XX WPI; 2002-508120/54.
XX N-PSDB; ABK87137.
XX
PT Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes -
XX
PS Claim 53; Fig 12; 248pp; English.
XX
CC The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4
CC proteins are useful for imaging vascular endothelium in the body of
CC an individual, and for diagnosing and treating a proliferative
CC disease or condition involving the vascular endothelium (preferably,
CC neovasculature) such as cancer, psoriasis, diabetic retinopathy,
CC atherosclerosis or menorrhagia. The ECSM4 proteins are also useful in
CC the manufacture of diagnostic or prognostic agent for such conditions.
CC The proteins are also useful for detecting endothelial damage or
CC activation, detecting a tumour or tumour neovasculature, cardiac
CC disease, or endometriosis by detecting the amount of ECSM4 present in
CC a sample. The polynucleotide sequences encoding ECSM4 are useful in
CC gene therapy for treating a hypoxic condition such as cancer, cardiac
CC disease, endometriosis or atherosclerosis and in the manufacture of
CC medicaments for treating the above disease. The sequences are useful
```

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XX WPI; 2002-599716/64.
DR N-PSDB; ABQ92573.
XX
XX New polynucleotides and polypeptides useful for diagnosing, prognosing,
PT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders
XX
XX Claim 11; Fig 1; 785pp; English.
XX
XX The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
XX Sequence 303 AA;
XX
XX Query Match 99.6%; Score 1602; DB 23; Length 303;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-132;
XX Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MGSGDLSLGGGSLPLLLLLLIMGMAQDSPQILVHPQDLFOGPGPARMSCRASGPP 60
DB 1 MGSGDLSLGGGSLPLLLLLLIMGMAQDSPQILVHPQDLFOGPGPARMSCRASGPP 60
XX
QY 61 PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGYVTCESNRL 120
DB 61 PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGYVTCESNRL 120
XX
QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
DB 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180
XX
QY 181 QPGRHTVSGSLLMARAEKSDXTVMCVATNSAGHRESRAARVSIQEPDYTEPVELLAV 240
DB 181 QPGRHTVSGSLLMARAEKSDXTVMCVATNSAGHRESRAARVSIQEPDYTEPVELLAV 240
XX
QY 241 RIQENVTLNPDPAEGPKPRPAVWLXWVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
DB 241 RIQENVTLNPDPAEGPKPRPAVWLXWVSGPXRLPNLTRPCSGPRLPREARELRGQR 300
XX
QY 301 NTG 303
DB 301 NTG 303
XX
RESULT 2
AA12934
ID AA12934 standard; Protein; 304 AA.
XX
XX AA12934;
XX
XX 17-JUN-1999 (first entry)
XX
XX Amino acid sequence of a human secreted peptide.
XX
XX Human secreted protein; cancer; immune disorder; infection;
XX inflammatory disorder; skin disorder; tumour; atherosclerosis;
XX restenosis; autoimmune disorder; Alzheimer's disease;
XX peripheral neuropathy; trauma; spinal cord injury; allergy;
XX hematopoietic disorder; skeletal disorder; neurological disorder;
```

arthritic disorder; asthma; immunodeficiency disease; AIDS;  
transplant rejection; ss.

Homo sapiens.

Key Location/Qualifiers  
Peptide 1..27  
Protein /note= "signal peptide"  
28..303  
/note= "secreted protein"

WO9911293-A1.

11-MAR-1999.

03-SEP-1998; 98WO-US18360.

12-SEP-1997; 97US-0058974.

05-SEP-1997; 97US-0057626.

05-SEP-1997; 97US-0057663.

05-SEP-1997; 97US-0057669.

12-SEP-1997; 97US-0058666.

12-SEP-1997; 97US-0058667.

12-SEP-1997; 97US-0058973.

(HUMA-) HUMAN GENOME SCI INC.

Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS;

Rosen GA, Ruben SM, Shi Y;

WPI; 1999-204988/17.

N-PSDB; AAX51721.

New isolated human genes and the secreted polypeptides they encode

- useful for diagnosis and treatment of e.g. neurological disorders,

tumours, immune disorders, inflammation or haematological disorders

Claim 11; Page 190-191; 215pp; English.

AA12914-68 represent human secreted proteins. The polypeptides and

their corresponding polynucleotides are useful for preventing,

treating or ameliorating medical conditions, e.g. by protein or gene

therapy. Pathological conditions can also be diagnosed by determining

the amount of the new polypeptides in a sample or by determining the

presence of mutations in the new polynucleotides. Specific uses are

described for each polynucleotide, based on which tissues they are

most highly expressed in, and include developing products for the

diagnosis or treatment of cancer, immune disorders, infection,

inflammatory disorders, skin disorders, tumours, atherosclerosis,

restenosis, autoimmune disorders, Alzheimer's disease, peripheral

neuropathies, trauma, spinal cord injuries, allergy, hematopoietic

disorders, skeletal disorders, neurological disorders, arthritic

disorders, asthma, immunodeficiency diseases, AIDS and transplant

rejection. The polypeptides are also useful for identifying their

binding partners.

Sequence 304 AA;

Query Match 99.6%; Score 1602; DB 20; Length 304;

Best Local Similarity 100.0%; Pred. No. 5.3e-132;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSGDLSLGGGSLPLLLLLLIMGMAQDSPQILVHPQDLFOGPGPARMSCRASGPP 60

DB 1 MGSGDLSLGGGSLPLLLLLLIMGMAQDSPQILVHPQDLFOGPGPARMSCRASGPP 60

QY 61 PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGYVTCESNRL 120

DB 61 PTIRLLNGQPLSMVPPDPHLLPDGTLILLQPPARGHAGDQALSTDLGYVTCESNRL 120

QY 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180

DB 121 GTAVSRGARLSVAVLRDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWKDGKPLAL 180

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 30, 2004, 15:44:59 ; Search time 39.2487 Seconds  
(without alignments)  
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Title: US-10-047-021-86  
Perfect score: 1608  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	99.6	303	23 ABP62033	Human secreted pro
2	1602	99.6	304	23 AAY12934	Amino acid sequenc
3	1444	89.8	1007	23 ABB97310	Novel human protei
4	1444	89.8	1104	23 AAU99419	Human ECSM4 protei
5	1436	89.3	792	22 AAB95515	Human protein sequ
6	1436	89.3	792	22 AAG67430	Amino acid sequenc
7	1337	83.1	985	20 AAY41716	Human PRO860 prote
8	1337	83.1	985	21 AAB44272	Human PRO860 (UNQ4
9	1337	83.1	985	21 ABU61102	Human PRO860 polyp

10	1332	82.8	480	22 AAU00501	Human TANGO 330 fo
11	1112.5	69.2	1015	23 AAU99420	Mouse ECSM4 protei
12	955	59.4	934	23 AAU00500	Human TANGO 330 fo
13	446.5	27.8	753	20 AAW83927	Human T85 protein.
14	446.5	27.8	753	24 ABU04090	Human expressed pr
15	446.5	27.8	1649	20 AAY08404	Human ROBO1 protei
16	446.5	27.8	1649	24 ABU04091	Human expressed pr
17	446.5	27.8	1651	20 AAY13566	Human Robo 1 polyp
18	446.5	27.8	1651	24 ABU04089	Human expressed pr
19	446.5	27.8	1651	24 ABU04092	Human expressed pr
20	446.5	27.8	1651	24 ABU04093	Human expressed pr
21	446.5	27.8	1651	24 ABU04094	Human expressed pr
22	405	25.2	1395	20 AAY13563	Drosophila Robo 1
23	405	25.2	1395	20 AAY08401	Drosophila sp. ROB
24	405	25.2	1395	22 ABB68257	Drosophila melanog
25	404.5	25.2	1515	23 AAO19185	Human neurotransmi
26	396.5	24.7	1422	23 AAO19179	Human neurotransmi
27	356.5	22.2	1297	20 AAY13565	C. elegans Robo po
28	356.5	22.2	1297	20 AAY08403	C. elegans Robo pr
29	345	21.5	1380	20 AAY08402	Drosophila sp. ROB
30	345	21.5	1381	20 AAY13564	Drosophila Robo 2
31	323	20.1	823	22 ABB13552	Drosophila melanog
32	307	19.1	885	22 ABB61502	Drosophila melanog
33	267.5	16.6	1496	20 AAW81030	Melanoma associate
34	267.5	16.6	1496	21 AAY70469	Human p53 target m
35	267.5	16.6	1496	24 ABU03498	Angiogenesis-associ
36	267.5	16.6	1498	22 ABB11587	Human peroxidasin
37	265.5	16.5	1463	23 AAO21660	Human secreted pro
38	260.5	16.2	937	22 AAM78714	Human protein SEQ
39	260.5	16.2	952	22 AAM78715	Human protein SEQ
40	260.5	16.2	1267	24 AAE32108	Human cytoskeleton
41	260.5	16.2	1359	24 AAE32109	Human cytoskeleton
42	260.5	16.2	1370	24 ABJ19347	NOVX related prote
43	259	16.1	1527	22 ABB57771	Drosophila melanog
44	254.5	15.8	3931	24 ABU07377	Human protein NOV9
45	253.5	15.8	793	23 AAE14781	Human immunoglobul

ALIGNMENTS

RESULT 1

ABP62033

ID ABP62033 standard; Protein; 303 AA.

AC ABP62033;

XX

DT 12-NOV-2002 (first entry)

XX Human secreted protein SEQ ID NO 86.

Human; notropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antineumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal; antiparasitic; cardiac; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.

XX Homo sapiens.

OS

XX WO200257420-A2.

XX 25-JUL-2002.

XX 17-JAN-2002; 2002WO-US01109.

XX 18-JAN-2001; 2001US-262066P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, LaFleur DW, Shi Y, Rosen CA, Olsen H;

XX Ebner R, Brewer LA;

XX

XX

XX

XX

XX



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